

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 10:57:38 ; Search time 225 Seconds  
(without alignments)  
7916.075 Million cell updates/sec

Title: US-10-088-726-25

Perfect score: 1002

Sequence: 1 atggagaggtggacatgaa.....ggttgaacagatctgggtaa 1002

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*
- 7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*
- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	229.4	22.9	2025	US-09-016-434-1482	Sequence 1482, Ap
2	229.4	22.9	2025	US-09-814-915A-74	Sequence 74, Appl
3	205.4	20.5	1842	US-08-442-134A-1	Sequence 1, Appl
4	205.4	20.5	1842	US-08-444-581B-1	Sequence 1, Appl
5	205.4	20.5	1842	US-08-446-088A-1	Sequence 1, Appl
6	180.2	18.0	1429	US-09-016-434-1068	Sequence 1068, Ap
7	180.2	18.0	1429	US-09-077-173D-1	Sequence 1, Appl
8	166.4	16.6	984	US-08-513-974B-57	Sequence 57, Appl
9	166.4	16.6	984	US-09-461-436B-57	Sequence 57, Appl
10	166.4	16.6	1023	US-08-513-974B-379	Sequence 379, App
11	164.8	16.4	1571	US-09-016-434-1108	Sequence 1108, Ap
12	158.4	15.8	984	US-08-459-046-1	Sequence 1, Appl
13	158.4	15.8	984	US-09-102-710B-1	Sequence 1, Appl
14	150.4	15.0	984	US-08-513-974B-41	Sequence 41, Appl
15	150.4	15.0	984	US-09-461-436B-41	Sequence 41, Appl
16	150.4	15.0	1020	US-08-513-974B-370	Sequence 370, App
17	99	9.9	1119	US-09-826-509-538	Sequence 538, App
18	99	9.9	1773	US-09-016-434-1405	Sequence 1405, Ap
19	97.4	9.7	998	US-08-432-174A-3	Sequence 3, Appl
20	94	9.4	1892	US-09-900-699A-1	Sequence 1, Appl
21	93.6	9.3	1475	US-08-097-938-1	Sequence 1, Appl
22	93.6	9.3	1475	US-08-476-000-1	Sequence 1, Appl
23	93.6	9.3	1475	US-08-472-840-1	Sequence 1, Appl
24	93.6	9.3	1475	US-08-476-976-1	Sequence 1, Appl

Sequence 1, Appl  
Sequence 1, Appl  
Sequence 60, Appl  
Sequence 60, Appl  
Sequence 60, Appl  
Sequence 60, Appl  
Sequence 568, App  
Sequence 60, Appl  
Sequence 13, Appl  
Sequence 1, Appl  
Sequence 1302, Ap  
Sequence 1456, Ap  
Sequence 31, Appl  
Sequence 181, App  
Sequence 1484, Ap  
Sequence 43, Appl  
Sequence 43, Appl  
Sequence 43, Appl  
Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-016-434-1482  
; Sequence 1482, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1482:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2025 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g984506  
US-09-016-434-1482

1/30/98 Jued.  
1/21/02 15..

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Query Match      22.9%; Score 229.4; DB 3; Length 2025;
Best Local Similarity 56.6%; Pred. No. 1.9e-51;
Matches 487; Conservative 0; Mismatches 366; Indels 8; Gaps 3;

Qy 43 TGCAGTCTTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTT 102
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 TGCCGCTTCAACGAGGACTTCAAGTACGTGCTGCTGTCTACGGCGTGGTGC 377
Qy 103 ATCTAGGGCTGCCACTAAATGGCACTGCTTGTGGCACTTCTGGGCGCAAAACAAGCGC 162
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 GTGCTTGGCTGTGCTGACGCCGTGGCGCTTACATCTTCTGTGGCGCTCAAGACC 437
Qy 163 TGGAGCTGTGCCACCACTATCTGTGTAACCTGATGGTGGCGACCTGCTTATGTGCTA 222
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
438 TGGAAATGGCTTCAACGAGGACTTCAAGTACGTGCTGCTGTCTACGGCGTGGTGC 497
Qy 223 T---TGGCCCTTCATCATCACTACTCTATATCAACCTTTACGGCAGCATCCTGCTGCTG 279
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
498 TCCCTGGCGCTGTGCTGTAACGCCGCTGGCGCTCTACATCTTCTGTGGCGCTCAAGACC 557
Qy 280 CTCTGAACTGTGTGCACTTCTCTTCTATATCAACCTTTACGGCAGCATCCTGCTGCTG 339
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
558 CTCTGCAAGCTGTGTGCTTCTCTTCTACACCACTTTTACTGCACTCTCTTCTCTC 617
Qy 340 ACCTGCACTCTGTGCACTTCTGTGTAACCTGATGGTGGCGACCTGCTGCTGCTGCTG 399
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 ACCTGCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 677
Qy 400 CGGACCGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 459
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
678 GGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 737
Qy 460 CTGCTGCCACACCTGCGCTTCTCCACAGGACTACATCAATGCGCAGATGATCTGCTAT 519
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
738 CAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Qy 520 GACATGACAGCCAGAGAAATTTTGTATCGGCTTTTGTGCTTACCGCATAGTCTGACATG 579
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
798 GACACCTTGGCACCAGGCTTCTGCGCGCTTCTGCGCGCTTACAGCTCAGTCTGCTGGC 857
Qy 580 TCTGGCTT--TCTTTTCTCTTGTGCTATTTTGTGCTGCTATTTTGTGCTGCTGCTGCTG 637
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
858 CTGCTCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917
Qy 638 CTGATCAAGCGCAGAGGAACTCATGAGGACAGGCAACACAGCCGAGCAGTCTCCATC 697
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918 CTGCTAAGCCAGGCTACGGGACCTCGGGCGGCTTCTAGGGCGCAAGCGCAAGTCCGTG 977
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
978 CGCACCATCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1037
Qy 758 CGCTCTTCTACCTACCATCTGCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGGCA 817
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1038 CGCACCTCTACTACTCTTCCGCT---CGGTGAGCTCTAGCTGCGCACCTCAAGGCC 1094
Qy 818 GCCAGTGTGGCTACAGATATGAGGCGCTTGTGAGTGTGAGCAGCTGCTCAAGCCCA 877
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1095 ATCAACTGGCTTCAAGGTTACCGCGCGCTGGCGAGTGTCAAGTGTGGCTTGACCCC 1154
Qy 878 GTCTGTACTTCTTTTCAAGG 898
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1155 GTGCTACTTCTGCTGGG 1175
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RESULT 2

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US-09-814-915A-74
; Sequence 74, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
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; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; TITLE OF INVENTION: Thereto
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814, 915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214, 870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 2025
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-915A-74
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Query Match      22.9%; Score 229.4; DB 3; Length 2025;
Best Local Similarity 56.6%; Pred. No. 1.9e-51;
Matches 487; Conservative 0; Mismatches 366; Indels 8; Gaps 3;

Qy 43 TGCAGTCTTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTT 102
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
318 TGCCGCTTCAACGAGGACTTCAAGTACGTGCTGCTGTCTACGGCGTGGTGC 377
Qy 103 ATCTAGGGCTGCCACTAAATGGCACTGCTTGTGGCACTTCTGGGCGCAAAACAAGCGC 162
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 GTGCTTGGCGTGTGCTGTAACGCCGCTGGCGCTCTACATCTTCTGTGGCGCTCAAGACC 437
Qy 163 TGGAGCTGTGCCACCACTATCTGTGTAACCTGATGGTGGCGACCTGCTTATGTGCTA 222
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
438 TGGAAATGGCTTCAACGAGGACTTCAAGTACGTGCTGCTGTCTACGGCGTGGTGC 497
Qy 223 T---TGGCCCTTCATCATCACTACTCTATATCAACCTTTACGGCAGCATCCTGCTGCTG 279
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
498 TCCCTGGCGCTGTGCTGTAACGCCGCTGGCGCTCTACATCTTCTGTGGCGCTCAAGACC 557
Qy 280 CTCTGCAAGCTGTGTGCACTTCTCTTCTATATCAACCTTTACGGCAGCATCCTGCTGCTG 339
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
558 CTCTGCAAGCTGTGTGCTTCTCTTCTACACCACTTTTACTGCACTCTCTTCTCTC 617
Qy 340 ACCTGCACTCTGTGCACTTCTGTGTAACCTGATGGTGGCGACCTGCTGCTGCTGCTG 399
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 ACCTGCACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 677
Qy 400 CGGACCGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 459
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
678 GGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 737
Qy 460 CTGCTGCCACACCTGCGCTTCTCCACAGGACTACATCAATGCGCAGATGATCTGCTAT 519
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738 CAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 797
Qy 520 GACATGACAGCCAGAGAAATTTTGTATCGGCTTTTGTGCTTACCGCATAGTCTGACATG 579
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
798 GACACCTTGGCACCAGGCTTCTGCGCGCTTCTGCGCGCTTACAGCTCAGTCTGCTGGC 857
Qy 580 TCTGGCTT--TCTTTTCTCTTGTGCTATTTTGTGCTGCTATTTTGTGCTGCTGCTGCTG 637
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
858 CTGCTCTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 917
Qy 638 CTGATCAAGCGCAGAGGAACTCATGAGGACAGGCAACACAGCCGAGCAGTCTCCATC 697
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
918 CTGCTAAGCCAGGCTACGGGACCTCGGGCGGCTTCTAGGGCGCAAGCGCAAGTCCGTG 977
Qy 698 CGGACCATCTACTGCTGTGTGGCTCTTACCCCTCTGTTTGTGGCTTCCATATCACT 757
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
978 CGCACCATCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1037
Qy 758 CGCTCTTCTACCTACCATCTGCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGGCA 817
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1038 CGCACCTCTACTACTCTTCCGCT---CGGTGAGCTCTAGCTGCGCACCTCAAGGCC 1094
Qy 818 GCCAGTGTGGCTACAGATATGAGGCGCTTGTGAGTGTGAGCAGCTGCTCAAGCCCA 877
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 1095 ATCAACATGGCGCTACAGGTTACCGCGCTGGCGAGTGTAAACAGTTGCTTGACCCC 1154  
Qy 878 GTCTGTACTTCTTTCAAGG 898  
Db 1155 GTGCTCTACTCTCTGGCTGGG 1175

## RESULT 3

US-08-442-134A-1  
; Sequence 1, Application US/08442134A  
; Patent No. 5596088  
; GENERAL INFORMATION:  
; APPLICANT: Boucher, Richard C.  
; APPLICANT: Weisman, Gary A.  
; APPLICANT: Turner, John T.  
; APPLICANT: Harden, Thomas K.  
; APPLICANT: Parr, Claude E.  
; APPLICANT: Sullivan, Daniel M.  
; APPLICANT: Erb, Laura  
; APPLICANT: Lustig, Kevin D.  
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and  
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bell, Seltzer, Park & Gibson  
; STREET: Post Office Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5596088th Carolina  
; COUNTRY: USA  
; ZIP: 28234

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/442,134A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5470-71A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-420-2200  
; TELEFAX: 919-881-3175  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1842 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 57..1181

US-08-442-134A-1

Query Match 20.5%; Score 205.4; DB 2; Length 1842;  
Best Local Similarity 56.4%; Pred. No. 5e-45;  
Matches 486; Conservative 0; Mismatches 361; Indels 14; Gaps 5;

Qy 43 TCCAGTCTCTAGAGTACAGGTTACCTCTCGCTGGCCTCAGTATCATCTTT 102  
Db 129 TGCCGCTTCAAGAGGACTTCAAGTACGTGTCTGCTGCTGTCTACGGGTGGTGTGC 188  
Qy 103 ATCTAGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGC 162  
Db 189 GTGCTTGGGCTGTGTCTGAACCCCTGGGCTCTTACATCTTCTGTGGCGCTCAAGACC 248  
Qy 163 TGGAGCTGTGCCACCACTATCTGGTGAACCTGTAGTGTGGCGGCACTGCTTTATGTGCTA 222  
Db 249 TGAATGGCTCCACACATATATGTTCCACCTGGCTGTGTGTGATGCACTGTATGGGCC 308

Qy 223 T---TGCCCTTCTCATCATCACTACTACTAGTACAGGTGGCCCTTTCGGGGAGCTG 279  
Db 309 TCCTTGGCGTGTGTCTATTACTAGCGCGGGGACCACTGGCCCTTCAGCACGGTG 368  
Qy 280 CTCTGCAAGCTGTGTGCACTCTCTTATATCAAACTTTACGGCAGATCTCTGCTGTG 339  
Db 369 CTCTGCAAGCTGTGTGCGCTCTCTTCTACACCAACTTTTACTGACGATCTCTTCTCTC 428  
Qy 340 ACCTGATCTCTGTGACACAGTTCTTAGGTGTGTGCCACCCACCTGTGTGCTGCCCTAC 399  
Db 429 ACCTGATCAAGCTGTGACCGGTGTCTGGGGCTCTTACGACCTCTGCGCTCTCTCGGCTGG 488  
Qy 400 CGGACCGCGAGGATGCTGCTGGGCAACGACCACTTGGGCGCTTGGTGGTCTCTCCAG 459  
Db 489 GGGCGGGCGCTACGCTCGCGGGTGGCGGGCGGTGTGGG---TGTGGTGTCTGSCC 545  
Qy 460 CTGTGCGCCACATGCGCTTCTCCCAAGGATATCAATATGCGCAGATCTGTGTAT 519  
Db 546 TGCAGGCGCGCTGTCTACTTTGTCAACCAAGCGCGGGCGGCTAACCTGCCAC 605  
Qy 520 GACATGACCGCAAGAGATTTTGTATCGGCTTTTTCCTACGGCATAGTTCTGACATTG 579  
Db 606 GACACCTCGGACCGGAGCTCTTACGCGCTTCTGGGCTTACAGTCTCATCTCTGGGC 665  
Qy 580 TCTGGCTT---TCTTTCCTCTCTTGGTGTCTTGTGTGTCTTACCTGATGGTCAGGAGC 637  
Db 666 CTGCTCTTGGGGTGGCTTGGCTCATCTTGTCTGTCTGTCTGCTCATGGCTCGGGGA 725  
Qy 638 CTGATCAAGCCAGAGAGAACCTCATGAGCAGGCAACAGCCGAGCGCAGGTCTCATC 697  
Db 726 CTGCTAAAGCCAGCTACGGGACCTCGGGGGCTGCTAGGGCAAGCGCAAGTCCGCTG 785  
Qy 698 CGGACCATCTACTGTGTGTGGCTCTTCACTCTCTGTTTGTGGCTTCCATCATCT 757  
Db 786 CGCACCATCGCGGT 845  
Qy 758 CGCTCTCTTACCTCAGCATCTCTCTTCTCTCAGGACTGCCAGCTCTTGTATGGCA 817  
Db 846 CGCACCTCTACTACTCTCTTCCGT---CGCTGACCTCAGTGGCCACACCTCAAGCC 902  
Qy 818 GCCAGTGTGGCTCAAGATATGAGGCGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 877  
Db 903 ATCAACATGGCTTACAGGT---TACCGGGTGGCCAGTGTCTAACAGTTGCTTGAACCC 959  
Qy 878 GTCTGTACTTCTTTCAAGG 898  
Db 960 GTGCTCTACTCTCTGGCTGGG 980

## RESULT 4

US-08-444-581B-1  
; Sequence 1, Application US/08444581B  
; Patent No. 5607836  
; GENERAL INFORMATION:

; APPLICANT: Boucher, Richard C.  
; APPLICANT: Weisman, Gary A.  
; APPLICANT: Turner, John T.  
; APPLICANT: Harden, Thomas K.  
; APPLICANT: Parr, Claude E.  
; APPLICANT: Sullivan, Daniel M.  
; APPLICANT: Erb, Laura  
; APPLICANT: Lustig, Kevin D.  
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and  
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Bell, Seltzer, Park & Gibson  
; STREET: Post Office Drawer 34009  
; CITY: Charlotte  
; STATE: No. 5607836th Carolina  
; COUNTRY: USA  
; ZIP: 28234

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,581B
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/442,134
FILING DATE: 16-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1842 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 57..1181
US-08-444-581B-1

Query Match 20.5%; Score 205.4; DB 2; Length 1842;
Best Local Similarity 56.4%; Pred. No. 5e-45;
Matches 486; Conservative 0; Mismatches 361; Indels 14; Gaps 5;

Qy 43 TGCCAGTCTTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTT 102
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 129 TGCCGCTTCAAGAGGACTCAAGTACGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 188
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Qy 103 ATCTAGGGCTGCCACTAAATGGCACTGTCTTGCGCACTTCTGGGGCCAAACCAAGCGC 162
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Qy 189 GTGCTTGGGCTGTGCTGAAGCGGCTGCGGCTCTACATCTTCTTGTGCGGCTCAAGACC 248
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Qy 163 TGGAGCTGTGCCACCACTATCTGTGAACCTGATGTGTGGCGACCTGCTTTATGTGCTA 222
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Qy 223 T---TGCCCTTCCTCATCATCACTCACTAGATGACAGGTGGCCCTTCGGGGAGCTG 279
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 280 CTCTGCAAGCTGTGTGCACTTCTCTGTCTATATCAACCTTTACGGCAGCATCCTGCTGCTG 339
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 369 CTCTGCAAGCTGTGTGCGCTTCTCTCTTCTACACCAACCTTTACTGACGATCCTTCTCTC 428
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 340 ACCTGCACTCTGTGCAACAGTTCCTAGGTGTGTGCCACCACTGTGTGCTGCCCTAC 399
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 429 ACCTGCACTGACGCTGCAACCGGTGTCTGGGGGTCTTACGACCTCTGCGCTCCCTGCGCTG 488
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 400 CGGACCCGCGGAGATGCTGTGCTGGGACCAAGCAACCACTGGGCGCTGTGCTCCAG 459
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 489 GGCGGGGCGCTGCTGCTGCGGGGTGGCGGGGCGGTGTGGG---TGTTGGTGTGCTGGCC 545
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 460 CTGCTGCCACACTGGGCTTCTCCACACGAGCTATACATCAATGGCCAGATGATCTGGTAT 519
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 546 TGCCAGGCGCGGTGCTACTTTGTCAACCAAGCGCGCGGCGCTAACCTGCCAC 605
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 520 GACATGTCAGCCAGAGAAATTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATG 579
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 606 GACACCTCGGACCCGAGCTCTTTCAGCGGCTTCTGTCGCTTACAGCTCAGTCTGCTGGGC 665
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 580 TCTGGCTT---TCTTTCCTCTCTTGGTGTGCTATTACCTGATGGTTCAGGAGC 637
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

666 CTGCTCTTTCGGGTGCCCTTTGGCGTTCATCTTGTCTGTACGTGCTCATGGCTCGCGGA 725
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
638 CTGATCAAGCCAGAGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATC 697
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
726 CTGCTAAAGCCAGCTACGGGACCTCGGGGGGCTGCTAGGGGCAAGCGCAAGTCCGTG 785
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
698 CGGACCATCTACTGTTGTGTGGCTTTCACCTCTGTTTGTGCTTGTGCTTGCATATCACT 757
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
786 CGACCATCGCGGTGGTGTGCTTTCGCGCTCTGCTTCCGCAATTCACAGTCACC 845
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
758 CGCTCCTTCTACCTCAACATCTGCTTCTTCTCAGGACTGCCAGCTCTTGATGGCA 817
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
846 CGACCTCTTACTACTCTTCCCT---CGTGGACCTGAGCTGCCACACCTCAAGGCC 902
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
818 GCCAGTGTGGCCTACAAGATATGAGGCGCTCTGGTGTGTGAGTGAGAGCTGCCCTCAACCA 877
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
903 ATCAACATGGCTTACAAGT---TACCGGCTGGCCAGTCTAAACAGTTGCTTGACCCC 959
Qy ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
878 GTCTGTACTTCTTTCAGG 898
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
960 GTGCTTACTTCTGCTGG 980

RESULT 5
US-08-446-088A-1
; Sequence 1, Application US/08446088A
; Patent No. 5691156
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5691156th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,088A
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1842 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 57..1181
; US-08-446-088A-1
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Qy	459	GTCGCTGCCACACATGCGCCTTCTCCACACGGACATACATCAATGGCCAGATGATCGGTA	518
Db	678	CCTCGTCCCAACCTGTTCTTTGTGTCACAACAGCAACAAAGGGACCAACCGCTCGTGGCCA	737
Qy	519	TGACATCAGCAGCCACAGAGAAATTTGATCGCTTTTGGCTACGGCATATGTTCTGCATTT	578
Db	738	TGACACACATCGGCCTCGAAGATTTGACCACTATGTGCATCTTACGCTCGCGGGTCATGGG	797
Qy	579	GTCTGGGCTTT--CTTTCCCTCTTTGGTCAATTTTGGTGTGCTATTCTACTGATGGTCAGGAG	636
Db	798	GCTGCTCTTTGGCGTGCCTGCCTGGTCACTCTTGTGTTGCTATGGACTCATGGCTCGTCG	857
Qy	637	CCTGATCAGCCAGAGAGAAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCAT	696
Db	858	CCTGTATCGCCCTTG-----CAGGCTCTGCAAGTCGTCTTCTCGCTCCGCTCTCT	911
Qy	697	CGGACCATCCTACTGGTGTGGCCCTCTTCACCCCTCTGTTTGTGGCTTCATATACAC	756
Db	912	CCGACCATAGCTGTGGTGTGACTGTCTTGTGTCGTCTGCTTCTGCGCTTTCACATCAC	971
Qy	757	TGGTCTCTTCTACCTCACCATCTGCTTTCTGCTTTTCTCAGGACATGCCAGCTCTTGATGGC	816
Db	972	CCGCACCAATTTACTACCTGGCCAGGCTGTTTGGAGCT---GACTGCCGAGTACTGAACAT	1028
Qy	817	AGCCAGTGTGGCCTPACAAGATATGGAGGCCTCTGGTGAGTGTGAGCAGCTGCCTCAACCC	876
Db	1029	TGTCAACGTGGTCTATAAGTGACTCGGCCCTCGCCAGTGTGCCAACAGCTGCCGTGATCC	1088
Qy	877	AGTCCTGTACTTCTTTCAAGGGGGGCAAAAATAGAGTCAGGCTCTCTCCAG	927
Db	1089	TGTGCTCTACTTGC--TCACTGGGGCAAAATATCGAGCTCAGTCTCGCTCAG	1137

## RESULT 7

```

US-09-077-173D-1
; Sequence 1, Application US/09077173D
; Patent No. 6790626
; GENERAL INFORMATION:
; APPLICANT: EUROSREEN S.A.
; APPLICANT: COMMUNI, DIDIER
; APPLICANT: PIROTTON, SABINE
; APPLICANT: PARMENTIER, MARC
; APPLICANT: BOEYNAEMS, JEAN-MARIE
; TITLE OF INVENTION: HUMAN PYRIMIDINE RECEPTOR
; FILE REFERENCE: 9409/2112
; CURRENT APPLICATION NUMBER: US/09/077,173D
; CURRENT FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/BE96/00123
; PRIOR FILING DATE: 1996-11-21
; PRIOR APPLICATION NUMBER: EPO 95870124.5
; PRIOR FILING DATE: 1995-11-21
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-077-173D-1

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RESIST 8

```

RESULI 8
US-08-513-974B-57
; Sequence 57, Application US/08513974B
; Patent No. 6114139
;
GENERAL INFORMATION:
;
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ontaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
;
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
;
; PRODUCTION, AND USE THEREOF
;
NUMBER OF SEQUENCES: 380
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;
STREET: 130 Water Street
;
CITY: Boston
;
STATE: MA
;
COUNTRY: USA
;
ZIP: 02109
;
COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235

REFERENCE/DOCKET NUMBER: 45753  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440

INFORMATION FOR SEQ ID NO: 57:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 984 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
US-08-513-974B-57

Query Match 16.6%; Score 166.4; DB 3; Length 984;  
Best Local Similarity 52.1%; Pred. No. 1.1e-34;  
Matches 445; Conservative 0; Mismatches 401; Indels 8; Gaps 3;

Qy 42 CTGCGAGTTCTCAGAGAGTCAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTT 101  
Db 51 CTGTCTCTACCGCGAGAACTTCAAGCAACTGTCTGTCCACCTGTGTATTCGGCGGTCT 110  
Qy 102 TATCTAGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGCGCAAAACCAAGCG 161  
Db 111 GCGGCTGGCTGCGGCTGAACATCTGTGTCAATTACCGAGATCTGCAGTCCCGCGGCG 170  
Qy 162 CTGGAGCTGTGCCACCACTATCTGGTGAACTGTAGTGTGGCCGACCTGCTTTATGTCT 221  
Db 171 CTGACCGCGCGCGGTGTACACCCCTAAACCTTGTCTGGCTGACCTGTATATATGCTG 230

Qy 222 AT---TGCCCTTCCTCATCATCATCACTACTACATAGATGACAGAGTGGCCCTTCGGGAGCT 278  
Db 231 CTCCCTGCCCTGCTCATCTAGAACTATGCCAAGGTGATCACTGGCCCTTTGGGACTT 290  
Qy 279 GCTCTGCAAGCTGTGTGCACTTCTCTGTCTATATCAACCTTTACGGCAGCATCTCTGTCT 338  
Db 291 CGCTGCGGCTGTGTGCGCTTCTCTTATGCAACCTTGCAACCTTGCAACCTTGCAACCT 350  
Qy 339 GACCTGCATCTCTGTGCACCAAGTTCTAGGTGTGTGCACCCACCTGTGTCTGCTGCCCTA 398  
Db 351 CACCTGCATCAGCTTCCAGCGCTACCTGGGCACTGCAACCCGCTGGCCCTTGCAAC 410  
Qy 399 CC---GGACCCGCGAGGATGCTGGCTGGGCAACCAACCACTGGGCGCTGGTGTCT 455  
Db 411 AGTGGGCGCGCGGCTGCTGGCTAGTGTGTAAACCGTGTGGCTGGCGGTGACAAC 470  
Qy 456 CAGCTGCTGCCACACTGGGCTTCTCCACAGGCACTACATCAATGGCCAGATGATCTG 515  
Db 471 CCAGTGGCTGCCACAGGCACTTCTGGCTGGCAAGGATCCAGCGTAAACCGCACTGCTG 530  
Qy 516 GTATGACATGACAGGCAAGAGAAATTTTGATCGGCTTTTGGCTACGCACTAGTCTTGAC 575  
Db 531 CTATGACCTCAGCCCGCTGCCCTGGGCAACCACTATATGCCCTATGGCATGGCTCTCAC 590  
Qy 576 ATTGTCTGGCTTTCT--TTCCCTCTTGGTCAATTTTGGTGTGTATTTCACTGATGGTCAG 633  
Db 591 TGTATCGGCTTCTGCTGCCCTTTGCTGGCTGCTGGCTGCTACTGTCTCTCTGGCCTG 650  
Qy 634 GAGCTGATCAAGCCAGAGAGAACTCTATGAGGACAGGCAACACAGCCCGAGCGAGTGC 693  
Db 651 CCGCTGTGGCGGAGGATGGCCCGGAGAGCTGTGGCCAGGAGCGGCGTGGCAAGGC 710  
Qy 694 CATCCGAGCACTCTACTGTGTGGCTTCTCACCTCTGTGTGGCTTGTGGCTTCTCCATAT 753  
Db 711 GCGCCGATGGCGGTGTGGCTGCTGCTTTGGCCATGAGCTTCTGCTCTTTTCACT 770  
Qy 754 CACTCGCTCTTTTACCTCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT 813  
Db 771 CACCAAGACAGCTTACCTGGCAGTGGCTCGACCGCGGCGTCCCTGCACTGATTGGA 830  
Qy 814 GGCAGCCAGTGTGGCTTACAGATATGGAGCCCTCTGTGTAGTGTGAGCAGCTGCTCAA 873  
Db 831 GGCCTTTGCGCGGCTTACAAAGGACGCGGCGCTTTGCCAGTGCACACAGCGTCTGGA 890  
Qy 874 CCCAGTCTGTACT 887  
Db 891 CCCATCTCTTCT 904

## RESULT 9

US-09-461-436B-57  
Sequence 57, Application US/09461436B  
Patent No. 6538107

GENERAL INFORMATION:  
APPLICANT: Shuji Hinuma

Yasuaki Ito  
Ryo Fujii

TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
Production, And Use Thereof

NUMBER OF SEQUENCES: 61

CORRESPONDENCE ADDRESS:

ADDRESSEE: Edwards & Angell, LLP

STREET: 101 Federal Street

CITY: BOSTON

STATE: MA

COUNTRY: USA

ZIP: 02209

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)

CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/461,436B
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-461-436B-57

Query Match          16.6%; Score 166.4; DB 3; Length 984;
Best Local Similarity 52.1%; Pred. No. 1.le-34;
Matches 445; Conservative 0; Mismatches 401; Indels 8; Gaps 3;

Qy 42 CTGCCAGTTCTCAGAGAGTACAGCAAGTCTACTCTCCCTGGCCCTACAGTATCATCTT 101
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 102 TATCTAGGCTGCGCACTAATGCGACTGCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 162 CTGGAGCTGTGCCACCACTATCTGTGGAACCTGATGCTGGCCGCACTGCTTTATGTGCT 221
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 171 CTTGACCCGACGCGCGGTACACCCCTAACTTGTCTGTGGTGAACCTGTATATGCTG 230
Qy 222 AT---TGCCCTTCTCATCATCATCTACTCATAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 231 CTCCTGCCCTGCTCATCTACAACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTT 290
Qy 279 GCTCTGAAGTGTGTCATCTTCTGTTCTATATCAACCTTTACGGGAGCATCTGCTGCT 338
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 291 CGCCTGGCGCTGCTGCTTCTTCTATGCAACCTGACGCGGAGCATCTCTTCTCCT 350
Qy 339 GACCTGCATCTCTGTGACCAAGTTCTTAGGTGTGTGCCACCCACTGTGTTCGCTGCCCTA 398
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 351 CACCTGCATCAGCTTCACGGCTACCTGGGCATCTGCCACCCGCTGGCCCTGGCAAA 410

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399 CC---GGACCCGACGAGCATGCCTGGCTGGGCACAGCAACCACTGGCCCTGGTGGTCCT 455
411 ACCTGGGGGGCGCGGCTGCCTGGCTAGTGTGTAAACCGTGGCTGGCCGCTGCAAC 470
456 CCAGCTGCTGCCACACACTGCGCTTCTCCACACGGACTACATCAATGGCCAGATGATCTG 515
471 CCAGTGCCTGCCACAGCCATCTTCGTGCGCAGGATCCAGGTAACCGCACTGTCTG 530
516 GTATGACATGACGACCAAGAGAAATTTGATCGGCTTTTTCCTACGGCATAGTTCTGAC 575
531 CTATGACCTCAGCCCGCTGCCCTGACCACTATATGCCCTATGGCATGGCTCTCAC 590
576 ATTGCTGGCTTCT---TTCCTCTCTTGGTCAATTTGGTGTGCTATTCATGATGTCAG 633
591 TGTCTCGGCTTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
634 GAGCTGATCAAGCCAGAGAGAACTCATGAGGACAGGCAACACAGCCGAGCGAGGTC 693
651 CCCTCTGTGCCGAGATGGCCGGGAGAGCTGTGGCCAGAGGGGGGGCTGGCAAGGC 710
694 CATCCGAGCATCTACTGTGTGTGGCTTTCACCTCTGTTTGTGGCTTTCATAT 753
711 GGCCCGCATGGCGTGTGTGGCTGCTGCTTTTGGCATCAGCTTCTGCTTTTTCAT 770
754 CATCGCTCTTCTACTCATCATCTGCTTCTGCTTCTGCTTCTCAGGACTGCCAGCTTCTGAT 813
771 CACCAAGACAGCCTACTTGGCAGTGGCTCGACCGCGGGCGTCCCTGCACTGTATTGGA 830
814 GGCAGCAGTGTGCTTACAGATATGGAGGCTCTGCTGAGTGTGAGCAGCTGCCCTCAA 873
831 GGCTTTGACGGCGCTTACAAAGGACGCGGCCGCTTTGCCAGTGCACAGCGTCTGGA 890
874 CCGAGTCTTCTACT 887
891 CCGCATCTTCT 904

RESULT 10
US-08-513-974B-379
; Sequence 379, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995

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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 379:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1023 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: fcdna  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 37..1020  
US-08-513-974B-379

Query Match 16.6%; Score 166.4; DB 3; Length 1023;  
Best Local Similarity 52.1%; Pred. No. 1.1e-34;  
Matches 445; Conservative 0; Mismatches 401; Indels 8; Gaps 3;  
QY 42 CTGCCAGTTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTT 101  
DB 87 CTGTGTCTACCGCGAGAACTTCAAGCAACTGTCTGCCACCTGTGTATTCCGGCGTCT 146  
QY 102 TATCTAGCGTGCACCTAAATGGCACTGTCTTGGCACTTCTGGGCGCAAAACCAAGCG 161  
DB 147 GCGCGCTGCGCTCGCGCTGAACATCTGTCTANTACCAAGATCTCCAGTCCCGCGGCG 206  
QY 162 CTGGAGCTGTGCAACACCTATCTGGTGAACCTGATGTGGCGGACCTGCTTTATGTCT 221  
DB 207 CTTGACCGCGACGCGCGGTACACCTTAAACCTTCTGTGGCTGACCTGTATATGCTG 266  
QY 222 AT---TGGCTTCTCATCATCACTACTACTAGATGACAGGTGGCGCTTGGGGAGCT 278  
DB 267 CTCCCTGCGCTGCTCATCACTAACAATGATGCCAAGGTGATCACTGGCGCTTTGGCGACTT 326  
QY 279 GCTCTGCAAGTGTGCACTTCTCTTATATCACTTTAGCGCAGCATCTGCTGCT 338  
DB 327 GCGCTGCGCGCTGGTCCGCTTCTCTTATATGCCAAGCTTGCACGCGAGCATCTTCTCT 386  
QY 339 GACCTGCATCTCTGTGCAACAGTCTCTAGGTGTGTGCCAACCCACCTGTGTGTGCTCCCTTA 398  
DB 387 CACCTGCATCAGTTCACGCGTACTCTGGGCATCTGCCACCGCTGGCGCCCTTGCACAA 446

QY 399 CC---GGACCGCAGGCGATGCTGCTGGGCGACACGACACACCTGGGCGCTGGTGGCTCT 455  
DB 447 ACGTGGGGGCGCGCGCTGCTGCTAGTGTGTAAACCGTGTGGCTGGCGGCTGACAAAC 506  
QY 456 CCAGCTGCTGCCACACACTGGGCTTCTCCACACAGGACTACATCAATGATGATGATGATG 515  
DB 507 CCAGTGGCTGCCACACAGGCTTCTGGCTGCGCACAGGATCCAGCGTAAACCGCACTGTCTG 566  
QY 516 GTATGACATGACGACGACGAGAAATTTGATGCGGCTTTTGGCTTACGCGCATAGTCTGAC 575  
DB 567 CTATGACCTCAGCGCGCTGCGCTGGCCACCCACTATATGCCCTATGGCATGGGCTCTCAC 626  
QY 576 ATTGTCTGGCTTCT---TTCCCTCTTGGTCAATTTTGGTGTGCTATTCACTGATGGTCTCAG 633  
DB 627 TGTATGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 686  
QY 634 GAGCCTGATCAAGCAGGAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCGAGTGC 693  
DB 687 CCGCTGTGCGCGCAGGATGGCGCGGAGAGCCCTGTGCGCCAGGAGCGGCTGGCAAGGC 746  
QY 694 CATCGGACCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753  
DB 747 GCGCGCATGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 806  
QY 754 CACTGCTGCTTCTACCTCACCATCTGCTTCTGCTTCTTCTCAGGACTGCCAGCTCTTGAT 813  
DB 807 CACCAAGACGCTTACCTGGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 866  
QY 814 GGCAGCCAGTGTGGCTTACAGATATGAGAGCCCTCTGCTGAGTGTGAGCAGCTGCTCAA 873  
DB 867 GGCCTTTGACGCGGCTTACAAAGGACGCGGCGCTTTGCCAGTGCACACAGCGTCTGGA 926  
QY 874 CCCAGTCTGTACT 887  
DB 927 CCCATCTCTTCT 940

## RESULT 11

US-09-016-434-1108  
Sequence 1108, Application US/09016434  
Patent No. 650938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1571 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: g1296659  
US-09-016-434-1108

Query Match 15.4%; Score 164.8; DB 3; Length 1571;  
Best Local Similarity 52.0%; Pred. No. 3.7e-34;  
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

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Qy 42 CTGCCAGTTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 101
Db 327 CTGTGTCTACCGCAGAACTTCAAGCAACTGCTCTGCCACCTGTGTATTCGGGGGTGCT 386
Qy 102 TATCCTAGGGTGGCCACTTAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
Db 387 GGCGGCTGGCGTGGCTGAACATCTGTGTCATTACCAGATCTGCACGTCGCCGCGGCG 446
Qy 162 CTGGAGCTGTGCCACCACTATCTGTGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCT 221
Db 447 CCTGACCGCAGCGCCGCTGTACACCCATAACCTTTGCTCTGGCTGACCTGTATATGCTG 506
Qy 222 AT---TGCCCTTCTCATATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db 507 CTCCTGCCCCGTCTCATCTACAACTATGCCAAGTGATCACTGGCCCTTTTGGCGACTT 566
Qy 279 GCTCTGAAGTGTGTGCACTTCCTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCT 338
Db 567 CGCCTGCGCGCTGCTGCTGCTTCTTCTATATGCAACCTTGCACGGCAGCATCTCTTCTCT 626
Qy 339 GACCTGATCTCTGTGACCAAGTTCCTAGTGTGTGCCACCCACTGTGTCGTGCCCTA 398
Db 627 CACCTGATCAGCTTCCAGCGCTACCTGGGCATCTGCCACCCGCTGGCCCTGGGCACAA 686
Qy 399 CC---GGACCGCAGGCACTGCTGGCTGGGCAACAGCACCACCTGGCCCTGGTGTGCT 455
Db 687 ACGTGGGGCGCGCGCTGCTGGCTAGTGTGTAGCGTGTGCTGGCGGTGACAACT 746
Qy 456 CCAGCTCTGCTCCCACTGGCTTCTCCACAGCGACTATCAATGGCCAGATGATCTG 515
Db 747 CCAGTGTCTGCCACAGCCATCTTTCGCTGCCACAGGCATCCAGCGTAAACCGCACTGCTG 806
Qy 516 GTATGATGACGACGCAAGAAATTTTGTATCGGCTTTTGGCCCTACGCGCATGTCTTGAC 575
Db 807 CTATGACCTCAGCCCGCTGCTGCTGGCCACCCACTATATGCCCTATGCGATGGCTCTCAC 866
Qy 576 ATTGCTGGCTTCTCT---TTCCCTCTTGTGTCATTTTGTGTGCTTATTCATGATGTCAG 633
Db 867 TGTATCGCTTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 926
Qy 634 GAGCCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693
Db 927 CCGCCTGTGCGCCAGGATGSCCGGCGAGACCTGTGSCCCAGGAGCGGCTGTCGAAGGC 986
Qy 694 CATCCGACCATCTACTGTGTGTGGCTTTCACCCCTCTGTTTGTGCTGCTTCCATAT 753
Db 987 GGCCCGCATGGCCGCTGTGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1046
Qy 754 CACTGCTCTCTTCTACCTCACTATCTCTTCTCTTCTCTTCTCAGGACTGCGGCTCTTGAT 813
Db 1047 CACCAAGACGCTTACTGTGGAGTGGCTCGACGCCGGGGCTGCCCTGCACTGTATTTGA 1106
Qy 814 GGCAGCAGTGTGGCTTACAGATATGAGGCTCTTGTGAGTGTGAGCAGCTGCTGCTCAA 873
Db 1107 GGCTTTTGACGGGCTTACAAAGGCAACGGCCGCTTTGGCCAGTGTGCCAAGCGGTGCTGGA 1166
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Qy 874 CCCAGTCTCTACT 887
Db 1167 CCCATCTCTCTT 1180

RESULT 12
US-08-459-046-1
; Sequence 1, Application US/08459046
; Patent No. 6008039
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A No. 6008039el Human Purinergic P2U Receptor
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3330 Hillview Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,046
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0038 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 984 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: Placenta
; CLONE: 179696
; US-08-459-046-1
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Query Match 15.8%; Score 158.4; DB 3; Length 984;  
Best Local Similarity 51.5%; Pred. No. 1.6e-32;  
Matches 440; Conservative 0; Mismatches 406; Indels 8; Gaps 3;

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Qy 42 CTGCCAGTTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 101
Db 51 CTGTGTCTACCGGAGAACTTCAAGCAACTGTGCTCCCACTGTGTATTCGGGGGTGCT 110
Qy 102 TATCCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
Db 111 GGCGCCTGCCCTCCCGTGAACATCTGTGTATTACCCAGATCTGCACGTCGCCGCGGCG 170
Qy 162 CTGGAGCTGTGCCACCACTATCTGTGTGAACCTGTGGTGGCGGACCTGCTTTATGTGCT 221
Db 171 CTTGACCCGACGCGCGGTGTACACCCCTAAACCTTGTCTGCTGACCTGTATATGCTG 230
Qy 222 AT---TGCCCTTCTCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db 231 CTCCTTGGCCCTGCTCATCTACAACTATGCCAAGGTGATCATCTGGCCCTTTGGCGACTT 290
Qy 279 GCTCTGCAAGCTGGTGCATCTTCTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCT 338
Db 291 CGCTTGGCGCTGTGCTGCTTCTTCTTATGCAACCTGCACGGGAGGATCCTCTTCTCT 350
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Qy	339	GACCTGCATCTCTGTGCACCAAGTTCTTAGTGTGTGCCACCACTGTGTTCGTCTGCCCTA	398
Db	351	CACCTGCATCAGTCTCCAGCGCTACTCGGCATCTGCCACCGCGCTGGCCCTGTGCCACA	410
Qy	399	CC----GGACCCGCGAGCATGCTGTGCTGGGACACAGCACCACTGTGGCCCTGGTGGTCT	455
Db	411	ACGTGGGGCGCGCGGCTGCTGTGCTAGTGTGTAGCCGTGTGGCTGGCCGTGACAC	470
Qy	456	CCAGCTGTGCCCAACACTGGGCTTCTCCACACGGACTACATCAATGGCCAGATGATCTG	515
Db	471	CCAGTGCCTGCCACAGCCATCTTCGCTGCCACAGGCATCCAGCGTAACCGCACTGTCTG	530
Qy	516	GTATGACATGACACGACCAAGAGAATTTTGATCGGCTTTTGGCTTACGGCATAGTTCTGC	575
Db	531	TTATGACCTCAGCCCGCTGCCCTGGCCACCACTATATGCCCTATGGATGGCTCTCAC	590
Qy	576	ATTGTCTGGCTTTCT--TTCCCTCCTTGGTCATTTTGGTGTGCTATTCACTGATGGTCAG	633
Db	591	TGTATCGGCTTCTGTGCTGCCCTTTGCTGCCCTGCTGCTGGCTGCTACTGTCTCTCGCCG	650
Qy	634	GAGCCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGGCCGAGCAGTGC	693
Db	651	CCGCTGTGCGCCAGGATGGCCCGCAGAGCCTGTGGCCACAGGACGCGGTGGCAAGGC	710
Qy	694	CATCCGGACATCTACTGTGTGTGGCCCTTTCACCCCTCTCTTTTGTGGCCCTCCATAT	753
Db	711	GGCCCGCATGGCCGTGGTGGTGTCTGTCTTTGGCATCAGCTTCTCGCCCTTTTCACAT	770
Qy	754	CACTCGCTCTTCTACCTCACCATCTGTCTTTCTGTCTTTCTCAGGACTGCCAGCTCTTGAT	813
Db	771	CACCAAGACAGCTTACCTTGGCAGTGGCTTCGAGCCGGGGGTGCCCTGCATCTGTATTGA	830
Qy	814	GGCAGCCAGTGTGGCCTACAAGATATGGAGGCCCTCTGGTGTGTGTGAGCAGCTGCCTCAA	873
Db	831	GGCCTTTTGCAGGGCCTACAAAGGCACGCGGCCGTTTGCAGTGGCCACAGCGTGTGGA	890
Qy	874	CCCAGTCTCTTACT	887
Db	891	CCCCATCTCTTCT	904

RESULT 13

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US-09-102-710B-1
; Sequence 1, Application US/09102710B
; Patent No. 6479630
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Stuart, Susan G.
; TITLE OF INVENTION: A NOVEL HUMAN PURINERGIC P2U RECEPTOR
; FILE REFERENCE: PP-0038-1 DIV
; CURRENT APPLICATION NUMBER: US/09/102,710B
; CURRENT FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6479630 179696CB1
US-09-102-710B-1

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	Query Match	15.8%	Score 158.4;	DB 3;	Length 984;
	Best Local Similarity	51.5%	Pred. No. 1.6e-32;		
	Matches 440;	Conservative	0;	Mismatches 406;	Indels 8; Gaps 3;
Qy	42	CTGCCAGTTCTCAGAGAGTACAAGCAAGTCTACTCTCCCTGCCCTACAGTATCATCTT	101		
Db	51	CTGTGTCTACCGCAGAACTTCAAGCAACTCTCTCTCCCACTGTGTTATTCGGCGGTGCT	110		

Qy	102	TATCTAGGGCTGCCA	CTAAATGGCACTGTCTTGCGCACTTCTGGGGCCAAACCAAGCG	161
Db	111	GGCGCTCGCCCTCCCGCTGAACATCTGTGTCAATACCCAGATCTGCACGCTCCGCGGCG	170	
Qy	162	CTGGAGCTGTGCCACACCACTTATCTGGTGAACTGATGGTGGCCGACCTGCTTTAATGTGCT	221	
Db	171	CTTGACCCGACGGCGGTGTACACCCATAACCTTGTCTGCTGACCTGTGCTATATGCTGT	230	
Qy	222	AT---TGCCCTTCTCATCATCACTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCT	278	
Db	231	CTCCCTGCCCTGCTCATCTACAACATAGCCCAAGTGATCACTGGCCCTTTGGCGCAT	290	
Qy	279	GCTCTGAAGCTGTGTGACATCTTCCTGTTCTATATCAAACTTTACGGCAGCATCTGCTGCT	338	
Db	291	CGCTGCGCTGTGTGCGCTTCTCTTCTATGCCAACTGTGACGCGGAGGATCTCTTCT	350	
Qy	339	GACTGATCTGTGTGACCAAGTTTCTAGGTGTGTGCGCACCACTGTGTTCGCTGCCCTA	398	
Db	351	CACCTGATCAGCTTCAGCGCTACCTTGGGATCTGCCACCCGCTGGCCCCCTGGCAAA	410	
Qy	399	CC---GGACCCGCGAGGATGCTGGCTGGGCACCAAGCACCACTGGGCCCTTGGTGGTCT	455	
Db	411	ACGTGGGGCGCGCGGCTGCTGGCTAGTGTGTAGCGGTGTGGCTGGCGTGACAAC	470	
Qy	456	CGAGCTCTGCCACACATGGGCTTCTCCACAGGACATAATCAATGGCCAGATGATCTG	515	
Db	471	CCAGTGCTGCCACAGCATCTTCGCTGGCCACAGGCATCCAGCGTAACCGCACTGTCTG	530	
Qy	516	GTATGATCAGCAGCCAGAGAAATTTTGATCGGCTTTTGGCTACGCGCATAGTTCTGCAC	575	
Db	531	TTATGACCTCAGCCCGCTGCTGCCGCGCACCTATATGCGCTATGGGATGGCTCTCAC	590	
Qy	576	ATTGCTCGGCTTCTCT---TTCCCTCTTTGGTCAATTTGGTGTGCTATTCACTGATGGTCAG	633	
Db	591	TGTCATCGGCTTCTGTCTGCCCTTTGCTGGCTGCTGCTGGCTGCTACTGCTCTCTGGCCTG	650	
Qy	634	GAGCTGATCAAGCCAGAGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTC	693	
Db	651	CCGCTGTGCGCGCAGGATGGCCCGGAGAGCTGTGGCCCAAGGAGCGCGTGGCAAGCG	710	
Qy	694	CATCGGACCATCTACTGTGTGTGGCTTTCACCTCTGTTTGTGGCCCTTCCATAT	753	
Db	711	GGCCCGCATGGCGGTGTGTGGCTGTGTCTTTTGGCATCAGCTTCTGCTGCTTTTTCAT	770	
Qy	754	CACCTGCTCTTCTACTCTCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTTGTAT	813	
Db	771	CACAGACAGCCTACTTGGCAGTGCGCTCGACGCGGGCGTCCCTGCATGTATTGGA	830	
Qy	814	GGCAGCAGTGTGGCCTTACAAGATATGAGAGCCCTCTGTGTAGTGTGAGCAGCTGCTCAA	873	
Db	831	GGCCTTTGAGCGGCTTACAAAGGACGCGGCGCGTTTGGCAGTGCACAGCGTGTCTGGA	890	
Qy	874	CCGAGTCTCTACT	887	
Db	891	CCCATCTCTTCT	904	

RESULT 14

US-08-513-974B-41

; Sequence 41, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo

; APPLICANT: Ohtaki, Tetsuya

; APPLICANT: Fukusumi, Shoji

; APPLICANT: Ohgi, Kazuhiro

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

; PRODUCTION, AND USE THEREOF

; NUMBER OF SEQUENCES: 380

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP



STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/513,974B  
FILING DATE: 14-SEP-1995  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 7-093989  
FILING DATE: 19-AUG-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 7-057186  
FILING DATE: 16-MAR-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1994  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 994 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-513-974B-41

Query Match 15.0%; Score 150.4; DB 3; Length 984;  
Best Local Similarity 50.9%; Pred. No. 2.2e-30;  
Matches 435; Conservative 0; Mismatches 411; Indels 8; Gaps 3;

Qy 42 CTGCAGTTCTCAGAGAAGTACAGCAAGTCTACTCTCCCTGGCCCTACAGATATCATCTT 101  
Dy 51 CTGGCTCTACCGTGAGGATTTCAAGCGACTGCTGCTAACCCCGGTATATCTCGGTGGTCT 110  
Qy 102 TATCCTAGGGTGCCTAAATGTCATCTGTTCTGTCGCACTTCTGGGGCCCAACCAAGCG 161

111 GGTGGTGGCCTGCCACTGCAATCTGGTCATCTGCCAGATCTGCCATCCCGCCGAC 170  
162 CTGGAGCTGTGCCACCACTTATCTGGTGAACCTGATGGTGGCCGCACTGCTTTATGTGCT 221  
171 CTTGACCCGTTCCGCTGTGTACACCTGAACCTGGCACTGGCGGACCTGATGTATGCTGTG 230  
222 AT---TGCCCTTCTCATCATCATCACTACTACTAGATGACAGGTGGCCCTTCGGGAGCT 278  
231 TTCACTACCCCTACTTATCTATAACTACGCGAGGGGACCACTGGCCCTTCGGAGACCT 290  
279 GCTCTCAAGCTGTGCACCTTCTGTTCTATATCAACCTTTTACGGCAGACATCTGCTGCT 338  
291 CGCTGCGGCTTTGTAGCTTCTCTCTATGCAATCTACATGGCAGCATCTCTGTTCT 350  
339 GACTGTCATCTCTGTGCACCACTTCTAGTGTGTGTCACCCACTGTGTTTCGCTGCCCTA 398  
351 CACTGCAITTAGCTTCCAGGCTACCTGGGCACTGCGCACCCCTTGGCTTCTGGCACAA 410  
399 CC---GGACCCGAGGATGCTGGTGGGCAACAGCACTGCGCCCTGGTGTGCT 455  
411 GCGTGGAGGTGCGCGTGTGCTGGGTAGTGTGGAGTGTGCTGGCTGGCTGTGACAGC 470  
456 CCAGCTGCTGCCACACACTGCGCTTCTCCACACGGACTACATCAATGGCCAGATGATCTG 515  
471 CCACTGCTGCCACCGGAGTCTTTGCTGCCACAGGATCCAGGCAACCGCACTGTGTG 530  
516 GTATGACATGACAGCAAGCAAGAGAAATTTGATCGGCTTTTTCCTACGGCATAGTTCTGAC 575  
531 CTACGACCTGAGCCCACTGCTACTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590  
576 ATTGTCTGGCT--TTCTTTTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633  
591 GGTGTCATGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 650  
634 GAGCTGTATCAAGCAGAGAGAGAACTCATGAGGACAGGCAACACACAGCCCGAGCCAGGTC 693  
651 CCGCTGTGTGCGCAGGATGGCCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 710  
694 CATCCGGAACCATCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 753  
711 GGCTCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 770  
754 CACTGCTGCTTCTACTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 813  
771 CACCAAGACAGCCTACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 830  
814 GGCAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 873  
831 GACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890  
874 CCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 904  
891 CCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

RESULT 15  
US-09-461-436B-41  
; Sequence 41, Application US/09461436B  
; Patent No. 6538107  
; GENERAL INFORMATION:  
; APPLICANT: Shuji Hinuma  
; Yasuaki Ito  
; Ryo Fujii  
; TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
; Production, And Use Thereof  
; NUMBER OF SEQUENCES: 61  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edwards & Angell, LLP  
; STREET: 101 Federal Street  
; CITY: BOSTON  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02209

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICANT: Patentin  
FILING DATE: 14-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/513,974  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
APPLICATION NUMBER: 7-093989  
FILING DATE: 19-APR-1995  
APPLICATION NUMBER: 7-057186  
FILING DATE: 16-MAR-1995  
APPLICATION NUMBER: 7-007177  
FILING DATE: 20-JAN-1995  
APPLICATION NUMBER: 6-326611  
FILING DATE: 28-DEC-1994  
APPLICATION NUMBER: 6-270017  
FILING DATE: 02-NOV-1994  
APPLICATION NUMBER: 6-236357  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-236356  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-189274  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189273  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189272  
FILING DATE: 11-AUG-1994

ATTORNEY/AGENT INFORMATION:  
NAME: CONLIN, DAVID G.  
REGISTRATION NUMBER: <Unknown>  
REFERENCE/DOCKET NUMBER: 45753 DIV2

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-439-4444  
TELEFAX: 617-439-4170

INFORMATION FOR SEQ ID NO: 41:  
SEQUENCE CHARACTERISTICS:

LENGTH: 984 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 41:

US-09-461-436B-41

Query Match i 15.0%; Score 150.4; DB 3; Length 984;  
Best Local Similarity 50.9%; Pred. No. 2.2e-30;  
Matches 435; Conservative 0; Mismatches 411; Indels 8; Gaps 3;  
QY 42 CTGCCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTT 101  
DB 51 CTGCGTCTACCGTGTAGGATTTCAAGCGACTGCTGCTAAACCCCGGTATCTCGGTGGTCT 110  
QY 102 TATCTAGGGTGGCCACTAAATGGCACTGTCTTGTGGCACTCTGGGGCCAAACCAAGCG 161  
DB 111 GGTGTGTGGCTGGCCACTGTGAACATCTGCGTCAATGCCAGATCTGGGCATCCCGCGGAC 170  
QY 162 CTGGAGCTGTGCCACCACTATCTGGTGAACCTGTAGTGGCCGACCTGCTTTATGTGCT 221  
DB 171 CCGTACCCGTTCCGCTGTGTACACCCCTGAACCTGGCACTGGCGGACCTGATGTATGCTG 230  
QY 222 AT---TGGCCTTCTCATCATCATCACTACTACTAGTACAGGTGGCCCTTGGGGAGCT 278  
DB 231 TTCACTACCCCTACTTATCTATACTACGACAGGGGACCACTGGGCCCTTGGGAGACCT 290  
QY 279 GCTCTGCAAGCTGGTGGCACTTCTCTTATATCAACCTTTACGGCAGCATCTCTGCTCT 338

Search completed: February 15, 2006, 11:15:14  
Job time : 227 secs

Db 291 CGCTGCGCGCTTTGTAGCTTCTCTTCTATGCAATCTACATGCGCAGCATCTCTGTTCTCT 350  
QY 339 GACTGTGATCTCTGTGACACAGTTTCTTAGGTGTGTGCCACCACTGTGTGCTGCGCTCA 398  
Db 351 CACCTGCATTAGCTTTCAGCGCTACCTGGGCACTGTGCCACCCCTGGCTTCTCTGGCAAA 410  
QY 399 CC---GGACCCGCGAGGATGCTGGCTGGGCAACAGACACCACTGGGGCCCTGGTGGTCT 455  
Db 411 GCGTGGAGGTGCGCGTCTGCTTGGGTAGTGTGTGGAGTCTGTGGCTGGCTGTGACAGC 470  
QY 456 CCAGTGTGTCGCCACACTGGGCTTCTCCCAACAGGACTATCAATAGGCCAGAGATGATCTG 515  
Db 471 CCAGTGTGTCGCCACAGGAGTCTTGTGTGTCACAGGCACTCCAGGCAACCCGACCTGTG 530  
QY 516 GTATGACATGACAGCCAGCAAGAGATTTGTATGGGCTTTTGGCTTACGCGATAGTCTTGAC 575  
Db 531 CTACGACCTGAGCCCAACCCATCTCTCTACTCTGCTACCTGCGTACCTGCGCTATGGGTATGGCCCTCAC 590  
QY 576 ATTGTCTGGCT--TTCTTTTCCCTCTTGGTCAATTTTGGTGTGCTATTTCACGTGAGTCTCAG 633  
Db 591 GGTCACTGGCTTCTTGTGCTGCGCTTCATAGCCTTACTGGCTTGTATTGTGCGATGGCCCG 650  
QY 634 GAGCCTGATCAAGCCAGAGGAGAACTCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693  
Db 651 CCGCTGTGTGCGCAGGATGGCCCGCAGAGGTCTCTGTGGCCCAAGAGCGCGCAGCAAGGC 710  
QY 694 CATCGGACCATCTACTGTGTGTGGCTTTCACCCCTCTGTTTGTGCTTCCATAT 753  
Db 711 GGCTCGTATGGCTGTGTGGTGGCAGCTGTCTTTGCCATCAGCTTCTTGGCTTCCACAT 770  
QY 754 CACTCGCTCTTCTACCTCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGAT 813  
Db 771 CACCAAGACAGCCTACTTGGCTGTGGCTCACGCCGGTGTCTCTTGGCTTGGCTGGA 830  
QY 814 GGCAGCCAGTGTGGCTTACAGATATGGAGCCCTCTGTGTAGTGTGAGCAGCTGCGCTCAA 873  
Db 831 GACCTTGGCTGTGCTTACAAAGGCACTGGGCCCTTGGCCAGTGTCAACAGTGTCTGGA 890  
QY 874 CCCAGTCTGTACT 887  
Db 891 CCCAATCTCTTCT 904

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:38:34 ; Search time 40 Seconds  
(without alignments)  
801.005 Million cell updates/sec

Title: US-10-088-726-20  
Perfect score: 1812  
Sequence: 1 MEKVDNMTSQGLCQFSEK.....NKLGEHPAGKRCFGLNRSG 333

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	402	22.2	328	2 155450	G protein-coupled
2	389.5	21.5	328	2 JC4800	P2Y6 receptor - hu
3	382.5	21.1	375	2 A54946	P-2U nucleotide re
4	379	20.9	373	2 A47556	ATP receptor P2u -
5	375	20.7	365	2 S68679	G protein-coupled
6	354	19.5	362	2 S33733	G protein-coupled
7	336	18.5	373	2 JC4737	G protein-coupled
8	334.5	18.5	373	2 JC4162	P2Y receptor - bov
9	290.5	16.0	308	2 I50241	G protein-coupled
10	282.5	15.6	344	2 T09508	intron 17 purinerg
11	263.5	14.5	370	2 T09508	heptahelical P2Y5-
12	259.5	14.3	353	2 JC2492	G protein-coupled
13	254	14.0	399	2 I48705	proteinase activat
14	249.5	13.8	359	2 S15403	angiotensin II rec
15	246.5	13.6	359	2 S44425	angiotensin II rec
16	246.5	13.6	420	2 I51667	thrombin receptor
17	244	13.5	359	2 JC1104	angiotensin II rec
18	242.5	13.4	397	2 S65188	proteinase-activat
19	241	13.3	359	2 I39418	angiotensin II rec
20	240	13.2	359	2 A48857	angiotensin II rec
21	239.5	13.2	359	2 A42656	angiotensin II rec
22	239	13.2	359	2 JH0621	angiotensin II rec
23	239	13.2	359	2 JC2134	angiotensin II rec
24	236.5	13.1	391	2 A39297	somatostatin recep
25	235.5	13.0	391	2 A41795	somatostatin recep
26	235.5	13.0	391	2 C41795	somatostatin recep
27	234.5	12.9	425	2 A37912	thrombin receptor
28	232.5	12.8	359	2 JC1194	angiotensin II rec
29	232.5	12.8	423	2 JC7677	allatostatin recep

ALIGNMENTS

RESULT 1

155450  
G protein-coupled P2 receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: 155450  
R:Chang, K.; Hanaoka, K.; Kumada, M.; Takuwa, Y.  
J. Biol. Chem. 270, 26152-26158, 1995  
A:Title: Molecular cloning and functional analysis of a novel P2 nucleotide receptor.  
A:Reference number: 155450; MUID:96064682; PMID:7592819  
A:Accession: 155450  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <RES>  
A:Cross-references: UNIPROT:Q63371; UNIPARC:UPI0000131003; GB:D63665; NID:G1066007; PID:N  
C:Superfamily: ATP receptor P2u  
C:Keywords: G protein-coupled receptor

Query Match 22.2%; Score 402; DB 2; Length 328;  
Best Local Similarity 32.5%; Pred. No. 2.8e-27;  
Matches 108; Conservative 53; Mismatches 137; Indels 34; Gaps 9;

Qy	1	MEKVDNMTSQEQL-----CQFSEKYKQVYLSLAYSIIIFILGLPLNGTVLWHFWMGTQKWS	56
Db	1	MER-DNGTIQAPGLPPTTCVYREDFKLLLPVSVVLVGLPLNVCVIAICASRRILT	59
Qy	57	CATTYLVNLMVADLLVYL-LPFLIITYSLDDRWPFGBELLCKLVHFLFYINLYGSILLTLC	115
Db	60	RSAYVTNLALADLLYACSLPLLIYNYARGDHPFGLACRLVRLFLFYANLHGSILFLTC	119
Qy	116	ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTWALVQLLPTLAFSTHDYINGOMIWD	174
Db	120	ISFQYILGICHPLAPMWHKRGGRRAAVVCGVYVWLVTAAQLPTAVFAATGQRNRTVCD	179
Qy	175	MTSQENFDRLFAYGIVLTLSGLF---SLIGHFGVFTDQGEQDQARCEHEDHSHSPSQ	230
Db	180	LSPPIILSTRILPYGMALTVIGFLPFTALLACYCRMARRLCRQDGPAGVQARRSKAAR	239
Qy	231	VHPDHPGTGVNPLPFCALPYHSLPLPHLL-SAFSGLPALDGSQCGLQDMSEAGECQL	289
Db	240	M-----AVVVAVFVISFLPFHITKTAYLAVRSTPGVSCPVLTEFAAAYKQTR	287
Qy	290	PQPS-----PVLSE-----KGGKRVRLLOKL	311
Db	288	PFASANSVLDPILFYFTQKFRQPHDLLOKL	319

RESULT 2

JC4800  
P2Y6 receptor - human  
C:Species: Homo sapiens (man)  
C:Date: 15-Oct-1995 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004

C;Accession: JC4800; G02514  
R;Communi, D.; Parmentier, M.; Boeynaems, J.M.  
Biochem. Biophys. Res. Commun. 222, 303-308, 1996  
A;Title: Cloning, functional expression and tissue distribution of the human P2Y6 receptor  
A;Reference number: JC4800; MUID:96222498; PMID:8670200  
A;Accession: JC4800  
A;Molecule type: mRNA  
A;Residues: 1-328 <CON>  
A;Cross-references: UNIPROT:Q15077; UNIPARC:UPI000005041C; EMBL:X97058  
A;Experimental source: Placenta  
R;Hammet, F.; Southey, M.C.; Somers, G.R.; Hutchins, A.M.; Venter, D.J.  
submitted to the EMBL Data Library, March 1996  
A;Reference number: H01373  
A;Accession: G02514  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 'M', 4-328 <HAM>  
A;Cross-references: UNIPARC:UPI000016B1B0; EMBL:U52464; NID:g1407632; PIDN:AA03572.1; F  
C;Genetics:  
A;Gene: P2Y6  
C;Superfamily: ATP receptor P2u  
C;Keywords: glycoprotein; placenta; receptor; transmembrane protein  
F;26-52/Domain: transmembrane #status predicted <TM1>  
F;63-86/Domain: transmembrane #status predicted <TM2>  
F;104-122/Domain: transmembrane #status predicted <TM3>  
F;143-167/Domain: transmembrane #status predicted <TM4>  
F;193-216/Domain: transmembrane #status predicted <TM5>  
F;241-264/Domain: transmembrane #status predicted <TM6>  
F;283-305/Domain: transmembrane #status predicted <TM7>  
F;5.173/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 21.5%; Score 389.5; DB 2; Length 328;  
Best Local Similarity 32.7%; Pred. No. 3.4e-26;  
Matches 108; Conservative 42; Mismatches 143; Indels 37; Gaps 9;

Qy 5 DMNTSQOGL- ---CFSEKYKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWCATT 60  
Db 4 DNGTGQALGPPTTCVRENFKQLLPVVSVAUAGLPLNICVITQICTSRALITAV 63

Qy 61 YLVNLMVADLLYL- LPLFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSIILLTLCISVH 119  
Db 64 YTNLALADLLYACSLPLLIYVNAQGDHWPFGDFACRLVRFVYANLHGSILFTCISFQ 123

Qy 120 QFLGVCHPLCSLPY- TRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMITYDMSQ 178  
Db 124 RYLGIChPLAPWHKRGGRRAALVCVAVLAVTTQCLPTAFAATGIQRNRTVCYDLSPP 183

Qy 179 ENFDLPAYGIVLTLSGFL- ---SLLGHFGLVFTDQEPDQARGEPHEDRQSPSOVHPD 234  
Db 184 ALATHYMPYGNALTVIGFLPFAALLACYLLAC- -----FLCRQDGPAPVQAQ 231

Qy 235 HPTGWPLHPLFCALPYHSLLLPHLL- SAFSGLPALDQCGQLQDMASGECEQLPQP- 292  
Db 232 ERGKAARMVAWVAFAISFLPPIHPTKTAIVLAVRSTPGVPCV- -LEAFAAAYKGRTPF 289

Qy 293 -----SPVLSP- ---KGGKRVRLLOKL 311  
Db 290 ASANSVLDPILFVFTQKKFRRRPHELLOKL 319

RESULT 3  
A54946  
P-20 nucleotide receptor - human  
C;Species: Homo sapiens (man)  
C;Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 17-Mar-1999  
C;Accession: A54946  
R;Parr, C.E.; Sullivan, D.M.; Paradiso, A.M.; Lazarowski, E.R.; Burch, L.H.; Olsen, J.C.  
Proc. Natl. Acad. Sci. U.S.A. 91, 3275-3279, 1994  
A;Title: Cloning and expression of a human P-20 nucleotide receptor, a target for cystic  
A;Reference number: A54946; MUID:94211846; PMID:8159738  
A;Accession: A54946  
A;Status: preliminary  
A;Molecule type: mRNA; protein

A;Residues: 1-375 <PAR>  
A;Cross-references: UNIPARC:UPI0000145104; GB:U07225  
A;Note: Parts of this sequence were confirmed by protein sequencing  
C;Genetics:  
A;Gene: GDB:P2RY2; HP2U; P2U  
A;Cross-references: GDB:362713; OMIM:600041  
A;Map position: 11q13.5-11q14.1  
C;Superfamily: ATP receptor P2u  
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.1%; Score 382.5; DB 2; Length 375;  
Best Local Similarity 33.0%; Pred. No. 1.6e-25;  
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

Qy 15 CQFSEKYKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWCATTYLVNLMVADLLYL 74  
Db 25 CRNEDFKYLLPVSYGVVCLGLCLNAGVLYIFLCRLKTNASTTYMFHLAVSDSYAA 84

Qy 75 -LPLFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSIILLTLCISVHQLFGVCHPLCSLPY 133  
Db 85 SLPLLYVYARGDHWPFSTVLCKLVRFVLTNYLCISILFTLCISVHRCICLVLRPLSLRW 144

Qy 134 RTRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMITYDMSQENFDLPAYGIVLT 193  
Db 145 GRARYARRVAGAVVVLVLAQAPVLYFVTT- ARGPLTCHDTSAPELFSRFVAYSSVM- 201

Qy 194 SGFLSLGHFGVLF- -----TQGEPPDQARGEPHEDRQSPSOVHP 233  
Db 202 ---LGLL- -FAVPFAVLVCYVLMARRLLKPAYGTSG- -----GLPRAKRSVRT- 245

Qy 234 DHPGTGWPLHPLF- -CALPVH- -----SLLPHLLSAFSGLPALDQSGCGLQDM 281  
Db 246 -----IAVLAVFALCFPLPHVTRTYSPRSJDLTSCHTLNAIN- -----MAYKVTRLA 293

Qy 282 ASGECEQLPQSPVLSPFKGKRVRLLOKLQKRLGHEPA- GRKRCPLGNRS 332  
Db 294 SANS- -LDPVLYFLAGRLVRFARDAKP- PTGSPATPARRTIGLRRS 339

RESULT 4  
A47556  
ATP receptor P2u - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: A47556  
R;Lustig, K.D.; Shiao, A.K.; Brake, A.J.; Julius, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 5113-5117, 1993  
A;Title: Expression cloning of an ATP receptor from mouse neuroblastoma cells.  
A;Reference number: A47556; MUID:93281707; PMID:7685114  
A;Accession: A47556  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-373 <LUS>  
A;Cross-references: UNIPROT:P35383; UNIPARC:UPI0000027DFF; GB:L14751; NID:g309457; PIDN:  
C;Superfamily: ATP receptor P2u  
C;Keywords: transmembrane protein

Query Match 20.9%; Score 379; DB 2; Length 373;  
Best Local Similarity 31.8%; Pred. No. 3.2e-25;  
Matches 114; Conservative 42; Mismatches 114; Indels 88; Gaps 12;

Qy 15 CQFSEKYKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWCATTYLVNLMVADLLYL 74  
Db 25 CRNEDFKYLLPVSYGVVCLGLCLNAGVLYIFLCRLKTNASTTYMFHLAVSDSYAA 84

Qy 75 -LPLFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSIILLTLCISVHQLFGVCHPLCSLPY 133  
Db 85 SLPLLYVYARGDHWPFSTVLCKLVRFVLTNYLCISILFTLCISVHRCICLVLRPLSLRW 144

Qy 134 RTRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMITYDMSQENFDLPAYGIVLT 193  
Db 145 GRARYARRVAAVVMVLVLAQAPVLYFVTT- SVRGTRITRCHDTSAPELFSRFVAYSSVM- 202

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QY 194 SGFLSLGHFGVLF-----TDGQEPDQARGEHPEDRO--HSPSOV 231
DB 203 ---LGLL--FAVPFVILVCYVLMARRLLKPAYGTG-----GLPRAKRKSVRTIALV 250
QY 232 HPDHTGVWPLHPLFCALPYH-----SLLLPHLLSAFS-----GLPALDGSQCG 276
DB 251 ----LAVFAL----CFLPFHVRTLYYSFRSLDLSCHTLNAINMAYKITRPLASANS- 300
QY 277 LQDMEASGECEQLPOPSVLSFKGKNRVLLQKLR-----QNKLGHEHPAGR 323
DB 301 -----LDPVLYFLAQQLRVRFARDAKPTEPTPSQARRKGLGHRPNR 343

RESULT 5
S86679
G protein-coupled receptor - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68679
R:Stam, N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
FEBS Lett. 384, 260-264, 1996
A:Title: Molecular cloning and characterization of a novel orphan receptor (P(2P)) expressed in rat brain
A:Reference number: S68679; MUID:96197801; PMID:8617367
A:Accession: S68679
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-365 <STA>
A:Cross-references: UNIPROT:P51582; UNIPARC:UPI000002E776; EMBL:X96597; NID:g1296631; PDB:1YUW
A:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor

Query Match 20.7%; Score 375; DB 2; Length 365;
Best Local Similarity 41.7%; Pred. No. 6.9e-25;
Matches 80; Conservative 30; Mismatches 74; Indels 8; Gaps 3;

QY 15 CQFSKYQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLVYL 74
DB 27 CWFDEDFKILLPVSYAVVFLGLGNAPTLWLFIRLRPMDATATYMFHLASTLTVL 86

QY 75 -LPFLIITYSLDDRWPFGELCKLVHFLFYINLYSGIILLTTCISVHQFLGVCHPLCSLPY 133
DB 87 SLPTLIYYAAHNHPFPGTEICKFVRFLFYWNLYGSLVFLTTCISVHRVILGICHPLRALRW 146

QY 134 RTRRHAWLGTSTWALVQLLPTLAFSHTDYINGQMIWYDMSQENFDRLPAYGIVLTL 193
DB 147 GRPLRAGLLCLAWLVWAGCLVPLNFVFTTSNKGTTVLCHDTRPEEDHYVHS----- 201

QY 194 SGFLSLGHFGV 205
DB 202 SANVGLL--FGV 211

RESULT 6
S33733
G protein-coupled receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33733
R:Webb, T.E.; Simon, J.; Krishnak, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock, P.
FEBS Lett. 324, 219-225, 1993
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A:Reference number: S33733; MUID:93285340; PMID:8508924
A:Accession: S33733
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <WEB>
A:Cross-references: UNIPROT:P34956; UNIPARC:UPI00000405D4; EMBL:X73268; NID:g395084; PDB:1YUW
A:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.5%; Score 354; DB 2; Length 362;
Best Local Similarity 30.8%; Pred. No. 4.5e-23;
Matches 98; Conservative 49; Mismatches 127; Indels 44; Gaps 10;
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QY 25 YLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLVYL--LPFLIITYS 83
DB 42 YLPTVYIILVFTIFGLGNSVAIWMFVHRPWSGIVSYMFNLALADFLVLTLPALIFYFF 101
QY 84 LDDRWPFGELCKLVHFLFYINLYSGIILLTTCISVHQFLGVCHPLCSLPYRTRRHAWLGT 143
DB 102 NKTDWIFGDVNMCKLQRFIFHVNLYGSLFLTTCISVHRVYGVVHPLKSLGRLKKNAVYVS 161
QY 144 STTWALVQLLPTLAFSHTDYINGQMI--WDYDMSQENFDRLPAYGIVLTL-----SGFLS 198
DB 162 SLVWALVAVIAPILFYSGTGVRRNKTTITCYDTTADAYLRSYFVYSMTCTTFMFCIPFTV 221
QY 199 ILGHFGVLTGQEPDQARGEHPEDRQHSQSVHFDHPGTGVWPLHPLFCALPVHSL--LPL 257
DB 222 ILGCYGLI-----VKALIYKLDNSPLRRK-----SIYLVIVLTVFAVSILP 264
QY 258 HHLASAFSGLPALD---GSQCGLQD-----MEASGECEQLPOPSVLSFKGKN 303
DB 265 FHVMTLNLRARLDFTQPMCAFNDKVATYQVTRGLASLNSC-----VDPILYFLAGDT 319
QY 304 -RVRLQLKLRQNKLGHEHP 320
DB 320 FRRRLSRATKRKSRSESP 337

RESULT 7
JC4737
G protein-coupled receptor P2Y1 - human
N:Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C:Species: Homo sapiens (man)
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC4737; JC4615; S54253
R:Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A:Title: Cloning and tissue distribution of the human P2Y1 receptor.
A:Reference number: JC4737; MUID:96205320; PMID:8630005
A:Accession: JC4737
A:Molecule type: DNA
A:Residues: 1-373 <JAN>
A:Cross-references: UNIPROT:P47900; UNIPARC:UPI0000001C06; GB:S81950; NID:g1839438; PDB:1YUW
R:Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Achwal, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A:Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A:Reference number: JC4615; MUID:96158962; PMID:8579591
A:Accession: JC4615
A:Molecule type: mRNA
A:Residues: 1-373 <AYY>
A:Cross-references: UNIPARC:UPI0000001C06; GB:U42029; NID:g1147730; PIDN:AAA97872.1; PFI:
A:Experimental source: erythro leukemia cells
R:Leon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A:Description: Cloning of a human putative P2Y receptor.
A:Reference number: S54253
A:Accession: S54253
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137,139-373 <LEO>
A:Cross-references: UNIPARC:UPI000016A5B9; EMBL:Z49205; NID:g798835; PIDN:CAA89066.1; PFI:
C:Comment: This receptor belongs to a family of G protein-coupled receptors. It respond
C:Genetics:
A:Gene: P2Y1; GDB:P2RY1
A:Cross-references: GDB:677125; OMIM:601167
A:Map position: 3pter-3qter
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein
F:52-77/Domain: transmembrane #status predicted <TM2>
F:88-111/Domain: transmembrane #status predicted <TM3>
F:124-152/Domain: transmembrane #status predicted <TM4>
F:171-191/Domain: transmembrane #status predicted <TM5>
F:214-237/Domain: transmembrane #status predicted <TM6>
F:261-282/Domain: transmembrane #status predicted <TM6>
F:305-328/Domain: transmembrane #status predicted <TM7>
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N:Alternate names: G-protein coupled receptor

C:Species: Homo sapiens (man)

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004

C:Accession: T09508

R:Bohm, S.K.; Trumpff, A.; Khitin, L.M.; Kong, W.; Payan, D.G.; Bunnett, N.W.

submitted to the EMBL Data Library, April 1997

A:Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene.

A:Reference number: Z16705

A:Accession: T09508

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-344 <BO>

A:Cross-references: UNIPROT:P43657; UNIPARC:UPI000005041B; EMBL:AF000546; NID:g2232068;

C:Genetics:

A:Map position: 13

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 15.6%; Score 282.5; DB 2; Length 344;  
Best Local Similarity 34.3%; Pred. No. 6.8e-17;  
Matches 71; Conservative 39; Mismatches 76; Indels 21; Gaps 7;

QY 4 VDMNTSQBGLQCFSEKQVYSLAYSIIFILGLPLNGTVMWHFWGQTKMWCATTYLV 63

Db 2 VSVNSH---CFYNDSEKTYLGYCMFVSVFVGLVSNCAIYIFICVLKVRNETTYMI 57

QY 64 NLWVADLLVYL-LPFLIITYSLDDRWPGELLCKLVHFLFYINLYGSIILLTICISVHQL 122

Db 58 NLAMSDLLFVFTLPRIE-YFTTRNWPFGDLCKISVNLFTYNNYGSILFTICISVDRL 116

QY 123 GVCHPLCSLPYRTRRHAWLGTSTWALVVLQLLPT--LAFSHDTYINGQMIWDMTSEN 180

Db 117 AIYVPEKSLTKTKNAKIVCTGWLTVIGSAPAVFQSTHSQGNASEACF-----EN 171

QY 181 FD----RLFAYGIVLTSLGFLSLGHF 203

Db 172 PPEATWKTYLSRIVI---FIEIVGFF 194

RESULT 11

JC5549

heptahelical P2Y5-like receptor - human

C:Species: Homo sapiens (man)

C>Date: 02-Sep-1997 #sequence\_revision 05-Sep-1997 #text\_change 09-Jul-2004

C:Accession: JC5549

R:Janseens, R.; Boeynaems, J.M.; Godart, M.; Communi, D.

Biochem. Biophys. Res. Commun. 236, 106-112, 1997

A:Title: Cloning of a human heptahelical receptor closely related to the P2Y5 receptor.

A:Reference number: JC5549; MUID:97366605; PMID:9223435

A:Accession: JC5549

A:Molecule type: DNA

A:Residues: 1-370 <JAN>

A:Cross-references: UNIPROT:Q99677; UNIPARC:UPI000016A4CA; DBJ:AF005419; NID:g2240034;

C:Superfamily: ATP receptor P2u

Query Match 14.5%; Score 263.5; DB 2; Length 370;

Best Local Similarity 34.0%; Pred. No. 3.3e-15;

Matches 69; Conservative 34; Mismatches 89; Indels 11; Gaps 4;

QY 5 DNMTSQEQGL-----CFSEKQVYSLAYSIIFILGLPLNGTVMWHFWGQTKMWS 56

Db 13 DSNLSRLPRLGNATANTTCIVDDSKYNLNGAVISVVFILGITSVLSLVFCFPMKWS 72

QY 57 CATTYLVNLMVADLLVYL-LPFLIITYSLDDRWPGELLCKLVHFLFYINLYGSIILLTIC 115

Db 73 ETAFITNLAVSDLLFVCTLPKIF-YNPNRWHPFGDTLKISGTAFTNIYGSMLFTLC 131

QY 116 ISVHQLGVCHPLCSLPYRTRRHAWLGTSTWALVVLQLLPTLAFSHDTYINGQMIWDM 175

Db 132 ISVDRLFAIVYFRSRTTRTNSAIVCAVGWILVLSGGSASLSFTSTNNVNTATTCFEG 191

QY 176 TSQENFDR-LFAYGVLTSLGFL 197

Db 192 LSKRWKTYLSKITIFIEVVGFI 214

RESULT 12

JC2492

G protein-coupled receptor 1 - rat

N:Alternate names: GPR-1

C:Species: Rattus norvegicus (Norway rat)

C>Date: 16-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004

C:Accession: JC2492

R:Marchese, A.; Cheng, R.; Lee, M.C.; Porter, C.A.; Heiber, M.; Goodman, M.; George, S.P.

Biochem. Biophys. Res. Commun. 205, 1952-1958, 1994

A:Title: Mapping studies of two G protein-coupled receptor genes: An amino acid difference

A:Reference number: JC2492; MUID:95110347; PMID:7811287

A:Accession: JC2492

A:Molecule type: mRNA

A:Residues: 1-353 <MAR>

A:Cross-references: UNIPROT:P46090; UNIPARC:UPI000012BA30; GB:S74702; NID:g786483; PIDN:

C:Superfamily: G-protein-coupled receptor

C:Keywords: glycoprotein; lipoprotein; phosphoprotein; receptor; thiolester bond; transmembrane

F:74-94/Domain: transmembrane #status predicted <TM2>

F:112-133/Domain: transmembrane #status predicted <TM3>

F:134-135/Region: DR motif

F:155-175/Domain: transmembrane #status predicted <TM4>

F:209-229/Domain: transmembrane #status predicted <TM5>

F:246-266/Domain: transmembrane #status predicted <TM6>

F:295-306/Domain: transmembrane #status predicted <TM7>

F:14,273/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150,231/Binding site: phosphate (Thr) (covalent) (by protein kinase A) #status predicted

F:330/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 14.3%; Score 259.5; DB 2; Length 353;

Best Local Similarity 33.3%; Pred. No. 6.9e-15;

Matches 64; Conservative 35; Mismatches 68; Indels 25; Gaps 5;

QY 28 LAYSIIFILGLPLNGTVMWHFWGQTKMWCATTYLVNLMVADLLVYL-LPFLIITYSLDD 86

Db 43 LLYALAVLGLPGNAIVW-FMGFKWKKTVTTLWFLNLAIADFIPLVPLVYSVALSF 101

QY 87 RWPFGELLCKLVHFLFYINLYGSIILLTICISVHQLGVCHPLCSLPYRTRRHAWLGTSTT 146

Db 102 HWPFGRLCKLNSFIAQLNMFSSVFFLTIVISLDRIYIHLHPGLSHPHRTLKNSLLVLFV 161

QY 147 WALVVLQLLPTLAFSHDTYINGQMIWDMTSENFDRL-----FAYGIVLT 192

Db 162 WLLASLGGPPLYPRDTVEVNNRIICYN-----NFQYVELTMRHHVLTWVKFLFGYLLP 216

QY 193 L-----SGFLSL 200

Db 217 LLTWSVCYLCL 228

RESULT 13

148705

proteinase activated receptor 2 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C:Accession: 148705

R:Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.

J. Biol. Chem. 270, 5950-5955, 1995

A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and

A:Reference number: 148705; MUID:95197620; PMID:7890726

A:Accession: 148705

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-399 <RES>

A:Cross-references: UNIPROT:P55086; UNIPARC:UPI0000021CA2; EMBL:Z48043; NID:g663020; PID

C:Superfamily: ATP receptor P2u

Query Match 14.0%; Score 254; DB 2; Length 399;

Best Local Similarity 35.6%; Pred. No. 2.4e-14;

Matches 69; Conservative 34; Mismatches 79; Indels 12; Gaps 7;

QY 20 KYKOVLSLAYSIIFILGLPLNGTVMHFWGQTKRWSCATTYLVNLMVADLLVLLPPLI 79  
 Db 74 KLTTVFUPVYIIVFVIGLPSNGMALWIFRTKKKHPAVIYMANLADLLSVINPPLK 133  
 QY 80 ITYSL-DRRWPFGLLCKLVHFLFYINLYSILLTTCISVHQFVGCVCHPLCSLPYRTRRH 138  
 Db 134 ISYHLGNWVYGEALCKVLGFFYGNMYCSILFWTCLSVQRYWVIVNPM-GHP-RKAN 191  
 QY 139 AWLQTS-TTVALVQLLPTLAFSHDYINGQMI--WYDMTSQBNF-DRLPAYGIVLTLS 194  
 Db 192 IAVGSLAIWLLIFLWITPIYVMKQTIIPALNITTCHDVLPEBVLGDMFNFLSLAIG 251  
 QY 195 GFLSLGHFGVLFT 208  
 Db 252 VFL-----FPALLT 260  
 RESULT 14  
 S15403  
 angiotensin II receptor type 1 - bovine  
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Nov-1999  
 C:Accession: S15403  
 R:Sasaki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.  
 Nature 351, 230-233, 1991  
 A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angioten-  
 A:Reference number: S15403; MUID:91251900; PMID:2041569  
 A:Accession: S15403  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-359 <SAS>  
 A:Cross-references: UNIPARC:UPI000012568B; GB:X62294; NID:g43; PIDN:CAA44182.1; PID:g44  
 C:Superfamily: vertebrate rhodopsin

Query Match 13.8%; Score 249.5; DB 2; Length 359;  
 Best Local Similarity 31.0%; Pred. No. 5.2e-14;  
 Matches 63; Conservative 42; Mismatches 87; Indels 11; Gaps 4;  
 QY 6 MNTSQEQL-----QCFSEKYKQVYLSL--AYSIIIFILGLPLNGTVMHFWGQTKRWSC 57  
 Db 3 LNSTEDGIKRIODDCPKAGRHNVIIFVIMPTLSIIIFVVGIFGNSLVVIVYFYMKLKV 62  
 QY 58 ATTLYNLMVADLLVYL-LPFLIITYSLDDRWPFGLLCKLVHFLFYINLYSILLTTCI 116  
 Db 63 ASVFLNLALADLCFLTLPLWAVYTAMEYRWPFGNVLCKIASASVSFNLYASVFLLTCL 122  
 QY 117 SVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVQLLPTLAFSHDYINGQMIWYDMT 176  
 Db 123 SIDRYLAIVHPMKSLRRTMLVAKVTCIIWLLAGLASLPTIIRNVFFIENTNITVCAF 182  
 QY 177 SQENFDRLPAYGIVLT--LSGFL 197  
 Db 183 HYESQNSTLPVGLGLTKNIGFL 205  
 RESULT 15  
 S44425  
 angiotensin II receptor type 1 - dog  
 C:Species: Canis lupus familiaris (dog)  
 C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C:Accession: S44425  
 R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.  
 FEBS Lett. 343, 146-150, 1994  
 A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor w  
 A:Reference number: S44425; MUID:94222188; PMID:8168620  
 A:Accession: S44425  
 A>Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-359 <BUR>  
 A:Cross-references: UNIPROT:P43240; UNIPARC:UPI000012568C; PIDN:AAB30674.1; PID:g546569  
 A:Experimental source: liver  
 C:Superfamily: vertebrate rhodopsin

Query Match 13.6%; Score 246.5; DB 2; Length 359;  
 Best Local Similarity 30.5%; Pred. No. 9.5e-14;  
 Matches 62; Conservative 43; Mismatches 87; Indels 11; Gaps 4;  
 QY 6 MNTSQEQL-----QCFSEKYKQVYLSL--AYSIIIFILGLPLNGTVMHFWGQTKRWSC 57  
 Db 3 LNSTEDGIKRIODDCPKAGRHNVIIFVIMPTLSIIIFVVGIFGNSLVVIVYFYMKLKV 62  
 QY 58 ATTLYNLMVADLLVYL-LPFLIITYSLDDRWPFGLLCKLVHFLFYINLYSILLTTCI 116  
 Db 63 ASVFLNLALADLCFLTLPLWAVYTAMEYRWPFGNVLCKIASASVSFNLYASVFLLTCL 122  
 QY 117 SVHQFLGVCHPLCSLPYRTRRHAWLGTSTTWALVQLLPTLAFSHDYINGQMIWYDMT 176  
 Db 123 SIDRYLAIVHPMKSPVRRTMLMAKVTCIIWLLAGLASLPTIIRNVFFIENTNITVCAF 182  
 QY 177 SQENFDRLPAYGIVLT--LSGFL 197  
 Db 183 HYESQNSTLPVGLGLTKNIGFL 205  
 Search completed: February 13, 2006, 14:43:02  
 Job time : 41 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:35:44 ; Search time 232 Seconds  
(without alignments)  
1012.676 Million cell updates/sec

Title: US-10-088-726-20

Perfect score: 1812

Sequence: 1 MEKVDNMTSQBGLQCFSEK.....NKLGEHPAGRKRCPLNRSG 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1804	99.6	361	2	Q711G2 HUMAN
2	449	24.8	328	1	P2RY3 CHICK
3	449	24.8	328	1	P2RY3 MELGA
4	429	23.7	374	2	O57466 MELEAGRIS G
5	424	23.4	537	1	P2RY8 XENLA
6	422	23.3	537	2	Q7ZM07 XENLA
7	420.5	23.2	310	2	O4SELS TETNG
8	411	22.7	543	2	O5BJ79 XENTR
9	405.5	22.4	308	2	O4SELS TETNG
10	402	22.2	328	1	P2RY6 RAT
11	397	21.9	328	1	P2RY6 MOUSE
12	396	21.9	361	1	P2RY4 RAT
13	395.5	21.8	328	2	O5R5L5 PONPY
14	395.5	21.8	377	1	P2RY2 HUMAN
15	394	21.7	361	1	P2RY4 MOUSE
16	389.5	21.5	328	1	P2RY6 HUMAN
17	389.5	21.5	347	2	Q7Z2A4 BRARE
18	383.5	21.2	373	2	O5YA25 PIG
19	379	20.9	373	1	P2RY2 MOUSE
20	378	20.9	365	2	O4VBB8 HUMAN
21	376.5	20.8	302	2	Q4RP73 TETNG
22	375	20.7	365	1	P2RY4 HUMAN
23	375	20.7	365	2	O5O2W2 HUMAN
24	375	20.7	365	2	O4VBB7 HUMAN
25	375	20.7	365	2	O5JT22 HUMAN
26	374.5	20.7	374	1	P2RY2 RAT
27	371.5	20.5	349	2	Q6P852 XENTR
28	367	20.3	357	2	Q9DE05 RAJER
29	367	20.3	358	2	Q4SPQ4 TETNG
30	365	20.1	230	2	O5Y809 PIG
31	354	19.5	362	1	P2RY1 CHICK

32	354	19.5	362	1	P2RY1 MELGA	P49652 meleagris g
33	339	18.7	182	2	O5DKX2 PIG	O5dkx2 sus scrofa
34	337.5	18.6	361	2	Q90X57 XENLA	Q90x57 xenopus lae
35	337.5	18.6	373	1	P2RY1 CAVPO	P59902 cavia porce
36	337.5	18.6	373	1	P2RY1 RAT	P49651 rattus norv
37	336	18.5	373	1	P2RY1 HUMAN	P47900 homo sapien
38	335.5	18.5	268	2	O5DKX3 PIG	O5dkx3 sus scrofa
39	334.5	18.5	373	1	P2RY1 BOVIN	P48042 bos taurus
40	328	18.1	373	1	P2RY1 MOUSE	P49650 mus musculu
41	328	18.1	373	2	O544J5 MOUSE	O544j5 m adult mal
42	325.5	18.0	373	2	O5XX73 CANFA	Q5xx73 canis famli
43	325	17.9	373	2	Q8BMJ5 MOUSE	Q8bmj5 mus musculu
44	290.5	16.0	302	2	Q4S8W3 TETNG	Q4s8w3 tetraodon n
45	290.5	16.0	308	1	P2RY5 CHICK	P32250 gallus gall

## ALIGNMENTS

### RESULT 1

Q711G2 HUMAN  
ID Q711G2\_HUMAN PRELIMINARY; PRT; 361 AA.  
AC Q711G2;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Nucleoside/nucleotide receptor.  
GN Name=P2Y2-like;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Blood;  
RA Bruss M., Bonisch H., Kugelgen I.;  
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Blood;  
RA Bruss M.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ345013; CAC87811.1; -; Genomic DNA.  
DR GO; GO:0016021; C:integral to membrane, IEA.  
DR GO; GO:0045028; F:purinergic nucleotide receptor activity, G-. . .; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopn.  
DR InterPro; IPR002286; P2\_purinocptor.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHHODOPSN.  
DR PRINTS; PR01157; P2YPURNOCPTR.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 361 AA; 40633 MW; 3992A1A1EF512AFE CRC64;

Query Match 99.6%; Score 1804; DB 2; Length 361;  
Best Local Similarity 99.7%; Pred. No. 4.7e-125;  
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MEKVDNMTSQBGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLMHFWGQTKRWSGATT 60
DB	29	MEKVDNMTSQBGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLMHFWGQTKRWSGATT 88
QY	61	YLNLNMLVADLLYVLLPFLIIITYSLDDRPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 120
DB	89	YLNLNMLVADLLYVLLPFLIIITYSLDDRPFGLLCKLVHFLFYINLYGSIILLTTCISVHQ 148
QY	121	FLGVCHPLCSPYRTRRHAWLGTSTTVALVVLQLPLTLPFSTHTDYINGQMIWYDWTSGEN 180

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|||||
149 FLGVCHFLCSUPYRTRHAWLGTSTTVALVQLPILAFSHDTYINGQMIWDMTSQEN 208
|||||
181 FDLRFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPHEDRQHSQVHPDHPGTGV 240
|||||
209 FDLRFAYGIVLTLSGFLSLGHFGVLTGQEPDQARGEPHEDRQHSQVHPDHPGTGV 268
|||||
241 PLHLFLCALPYHSLLLPHLLLSAFSGLPALDGSQGLQDMEASGECQLPQSPVLSFKG 300
|||||
269 PLHLFLCALPYHSLLLPHLLLSAFSGLPALDGSQGLQDMEASGECQLPQSPVLSFKG 328
|||||
301 GKNVRLLQKLRQNKLGEPHAGRCPCPLNRSG 333
|||||
329 GKNVRLLQKLRQNKLGEPHAGRCPCPLNRSG 361
|||||

RESULT 2
P2RY3_CHICK
ID P2RY3_CHICK STANDARD; PRT; 328 AA.
AC Q98907;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN Name=P2RY3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=96319774; PubMed=8700132;
RA Webb T.E., Henderson D., King B.F., Wang S., Simon J., Bateson A.N.,
RA Burnstock G., Barnard E.A.;
RT "A novel G protein-coupled P2 purinoceptor (P2Y3) activated
RT preferentially by nucleoside diphosphates.";
RL Mol. Pharmacol. 50:258-265(1996).
CC -!- FUNCTION: Receptor for extracellular ADP > UTP = UDP. The
CC activity of this receptor is mediated by G proteins which activate
CC a phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; X98283; CAA66930.1; -; mRNA.
CC HSSP; P34996; 1DDD.
CC Ensembl; ENSGALG0000017327; Gallus gallus.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR002286; P2_purnocptor.
CC InterPro; IPR000371; P2Y3_purnocptor.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01065; P2Y3PRNOCPT.
CC PRINTS; PR01157; P2YPURNOCPTR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
CC Transmembrane.
KW TOPO_DOM 1 22 Extracellular (Potential).
KW TRANSMEM 23 43 1 (Potential).
KW TOPO_DOM 44 57 Cytoplasmic (Potential).
KW TRANSMEM 58 78 2 (Potential).
KW TOPO_DOM 79 96 Extracellular (Potential).
KW TRANSMEM 97 117 3 (Potential).
KW TOPO_DOM 118 139 Cytoplasmic (Potential).
KW TRANSMEM 140 160 4 (Potential).
KW -----
```

```
FT TOPO_DOM 161 189 Extracellular (Potential).
FT TRANSMEM 190 210 5 (Potential).
FT TOPO_DOM 211 231 Cytoplasmic (Potential).
FT TRANSMEM 232 252 6 (Potential).
FT TOPO_DOM 253 275 Extracellular (Potential).
FT TRANSMEM 276 298 7 (Potential).
FT TOPO_DOM 299 323 Extracellular (Potential).
FT CARBOHYD 5 5 N-linked (GlcNAc.. ) (Potential).
FT DISULFID 94 172 By similarity.
SQ SEQUENCE 328 AA; 37587 MW; 7A3BF1C91F54FAAB CRC64;

Query Match 24.8%; Score 449; DB 1; Length 328;
Best Local Similarity 45.9%; Pred No. 4.3e-25;
Matches 85; Conservative 31; Mismatches 67; Indels 2; Gaps 2;

QY 15 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLMHFWGQTKRWSCATTYLVNLMVADLLYL 74
DB 13 CTFHEBFQVLLPLVYVSVFLLGLPLNAVVGQIWLARKALTRTTIYMLNMLAMADLLYVC 72
QY 75 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTCTSVHQFLGVCHPLCSL-P 132
DB 73 SLFLIYNYTKDYWPFGDFCKFVFQFYTNLHGSILFLTCTISVQRYMGICHPASWHK 132
QY 133 YRTRRHAWLGTSTTVALVQLLPTLAFSHDTYINGQMIWDMTSOENFDRLFAYGIVLT 192
DB 133 KKGKLUKTLVCAAVFIVIAQCLPTVFVFASTGTQRNRTVCYDLSPDRSTSYPPYGITLT 192
QY 193 LSGFL 197
DB 193 ITGFL 197

RESULT 3
P2RY3_MELGA
ID P2RY3_MELGA STANDARD; PRT; 328 AA.
AC O93361;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE P2Y purinoceptor 3 (P2Y3) (Nucleoside diphosphate receptor).
GN Name=P2RY3;
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RC NUCLEOTIDE SEQUENCE.
RP MEDLINE=98401046; PubMed=9730913;
RA Li Q., Oleesky M., Palmer R.K., Harden T.K., Nicholas R.A.;
RT "Evidence that the p2y3 receptor is the avian homologue of the
RT mammalian P2Y6 receptor.";
RL Mol. Pharmacol. 54:541-546(1998).
CC -!- FUNCTION: Receptor for extracellular UDP > ADP = UTP. The activity
CC of this receptor is mediated by G proteins which activate a
CC phosphatidylinositol-calcium second messenger system.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC EMBL; AF069555; AAC23863.1; -; Genomic_DNA.
CC HSSP; P34996; 1DDD.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC InterPro; IPR002286; P2_purnocptor.
CC InterPro; IPR000371; P2Y3_purnocptor.
CC Pfam; PF00001; 7tm.1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PRINTS; PR01065; P2Y3PRNOCPT.
CC PRINTS; PR01157; P2YPURNOCPTR.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
CC Transmembrane.
KW TOPO_DOM 1 22 Extracellular (Potential).
KW TRANSMEM 23 43 1 (Potential).
KW TOPO_DOM 44 57 Cytoplasmic (Potential).
KW TRANSMEM 58 78 2 (Potential).
KW TOPO_DOM 79 96 Extracellular (Potential).
KW TRANSMEM 97 117 3 (Potential).
KW TOPO_DOM 118 139 Cytoplasmic (Potential).
KW TRANSMEM 140 160 4 (Potential).
KW -----
```

InterPro; IPR000276; GPCR\_Rhodopsin.  
 InterPro; IPR002286; P2\_purinocptor.  
 InterPro; IPR000018; P2Y4\_purinocptor.  
 Pfam; PF00001; 7tm 1; 1.  
 PRINTS; PR00237; GPCRRHODOPSIN.  
 PRINTS; PR01066; P2Y4PRNOCPTR.  
 PRINTS; PR01157; P2YPURNOCPTR.  
 PROSITE; PS00237; G\_PROTEIN\_RECEPTOR\_1; UNKNOWN\_1.  
 PROSITE; PS0262; G\_PROTEIN\_RECEPTOR\_1.  
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
 SQ SEQUENCE 374 AA; 42594 MW; 849C465722BDD02B CRC64;

Query Match 23.7%; Score 429; DB 2; Length 374;  
 Best Local Similarity 40.8%; Pred.No.1.5e-23;  
 Matches 82; Conservative 40; Mismatches 71; Indels 8; Gaps 3;

Qy	8	TSEQGGLGCGSEKYSKVIVLSLAYSIIFILGLPLNGTVLWHEFGQTWRWSCATTLYLVLMV	67
Dd	26	TAAAEAKVFNEEFKEILLIPISYGIVFVVGLPUNSWAMMIFVSRRMPWNATITMFNLAI	85
Qy	68	ADLLYYVL-LPFALITYSLDORWPFGELLCCKLVHFLFYINLYSGIILLTTCISVHQFLGVCH	126
Dd	86	SDTLVYFSPLTVVYYADRNNPPFGVKVIKRVLFYANLYSSILFLTICSVHYRYMGICH	145
Qy	127	PLCSLPYRTERRHAWLTGTSTWALVQLVQLPTLAFSTHDYINGOMIYWMTSQNFOLFPA	186
Dd	146	FIRSLKWKTQHARLLCVGVMLVVTCLIPNLFIFFTSSKNDNSTLCHDTTKPEFDHYHV	205
Qy	187	YGVILTSLGSFLSLGHGFGLF 207	
Dd	206	YS-----SSIMALL--FGIPF 219	

RESULT 5  
 P2RY8\_XENLA STANDARD; PRT; 537 AA.

ID	P2RY8_XENLA	AC	P79928;
DI	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DE	10-MAY-2005	(Rel. 47, Last annotation update)	
DE	P2Y purinoceptor 8 (P2Y8).		
GN	Name=P2RY8;		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;		
OC	Xenopodinae; Xenopus; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RC	TISSUE=Neural plate;		
RC	MEDLINE=97284734; PubMed=9139711; DOI=10.1074/jbc.272.19.12583;		
RA	Bogdanov Y.D., Dale L., King B.F., Whitlock N., Burnstock G.;		
RT	"Early expression of a novel nucleotide receptor in the neural plate		
RT	of Xenopus embryos.";		
RL	J. Biol. Chem. 272:12583-12590(1997).		
CC	-1- FUNCTION: Receptor for extracellular ATP, UTP, CTP, GTP and ITP.		
CC	The activity of this receptor is mediated by G proteins which		
CC	activate a phosphatidylinositol-calcium second messenger system.		
CC	May play a key role in the early development of neural tissue.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use as long as its content is in no way modified and this statement is not		
CC	removed.		
CC	EMBL; X99953; CAA68213.1; -, mRNA.		
DR	HSP; P34996; 1DDD.		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	InterPro; IPR002286; P2_purinocptor.		
DR	InterPro; IPR000018; P2Y4_purinocptor.		

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DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01066; P2Y4RNOCPTR.
DR PRINTS; PR01157; P2Y4RNOCPTR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 49 Extracellular (Potential).
FT TRANSHEM 50 70 1 (Potential).
FT TOPO_DOM 71 79 Cytoplasmic (Potential).
FT TRANSHEM 80 100 2 (Potential).
FT TOPO_DOM 101 118 Extracellular (Potential).
FT TRANSHEM 119 139 3 (Potential).
FT TOPO_DOM 140 161 Cytoplasmic (Potential).
FT TRANSHEM 162 182 4 (Potential).
FT TOPO_DOM 183 210 Extracellular (Potential).
FT TRANSHEM 211 231 5 (Potential).
FT TOPO_DOM 232 254 Cytoplasmic (Potential).
FT TRANSHEM 255 275 6 (Potential).
FT TOPO_DOM 276 292 Extracellular (Potential).
FT TRANSHEM 293 316 7 (Potential).
FT TOPO_DOM 317 537 Cytoplasmic (Potential).
FT CARBOHYD 26 26 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 29 29 N-linked (GlcNAc...) (Potential).
FT DISULFID 116 193 By similarity.
SQ SEQUENCE 537 AA; 62024 MW; B2CF24812F3C19F2 CRC64;

Query Match 23.4%; Score 424; DB 1; Length 537;
Best Local Similarity 32.1%; Pred. No. 5e-23;
Matches 111; Conservative 59; Mismatches 138; Indels 38; Gaps 10;

Oy 3 KVDNN-TSQEGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTY 61
Db 22 KLLMNLNTDIEDICVDFEGFKLLPVSYSVAVFWGLPLNIAAMWIFIAKMRPNWPTTY 81

Oy 62 LVNLMVADLLVYL-LPFLIITYSLDDRPFGLLCKLVHFLFYINLYGSLILLCISVHQ 120
Db 82 MFNLALSDTLVLSLPTLVVYADKNWPFGEVLCKLVFLFYANLYSSILFLTCISVHR 141

Oy 121 FLGVCHPLCSLPYTRHAWLGSTTVALVVLQPLTLAGSHDTYINGQMWDYMTSQEN 180
Db 142 YRGVCHRTSLRRNNAKAYVICALVMSVTLCLVFNLIFFVSPKVNVICTHTTPED 201

Oy 181 FDLRFAY--GIVLTLSGF--LSLLGHFGVLFTDQGEPPDQARGEHEDRQHSQVHPDHP 236
Db 202 FARVVEYSTAIMCLLFGIPCLLIAGCYGLMRELKPIVS-----GNQQTLPYSKRSIK 256

Oy 237 TGVWPLHPLFCALPYHSLLLPHLLSAFSGLPALDGSQC-----GLQDMEASGE 285
Db 257 T-----IIFVMAFAICFMFPHITRTLYVYVARLLGKCYALNVINVTYKVTRELASANS 310

Oy 286 CEQLPQSPVLSF-KGGKNNRVLQKLQKRNKLGEHPAGRKRCPCGLN 330
Db 311 C-----IDPILYFLANDRYRRRLRTVRRRS-----SVPNRRQMTN 347

RESULT 6
O7ZWQ7 XENLA PRELIMINARY; PRT; 537 AA.
AC O7ZWQ7 XENLA PRELIMINARY;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE P2Y4-prov protein.
GN Name=p2ry4-prov.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
```

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RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; BC046837; AAH46837.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0045028; F: purinergic nucleotide receptor activity; G-...; IEA.
DR GO; GO:0004872; F: receptor activity; IEA.
DR GO; GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin...; IEA.
DR GO; GO:0007165; P: signal transduction; IEA.
DR InterPro; IPR002286; P2_purinocptor.
DR InterPro; IPR000018; P2Y4_purinocptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PRINTS; PR01066; P2Y4RNOCPTR.
DR PRINTS; PR01157; P2Y4RNOCPTR.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 537 AA; 61982 MW; B030F67D76CB9622 CRC64;

Query Match 23.3%; Score 422; DB 2; Length 537;
Best Local Similarity 32.1%; Pred. No. 7e-23;
Matches 110; Conservative 58; Mismatches 137; Indels 38; Gaps 10;

Oy 6 MN-TSQEGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVN 64
Db 25 MNLNTDIEDICVDFEGFKLLPVSYSVAVFWGLPLNIAAMWIFIAKMRPNWPTTYVNFN 84

Oy 65 LMVADLLVYL-LPFLIITYSLDDRPFGLLCKLVHFLFYINLYGSLILLCISVHOFGL 123
Db 85 LALSDDLTVLSLPTLVVYADKNWPFGEVLCKLVFLFYANLYSSILFLTCISVHYRG 144

Oy 124 VCHPLCSLPYTRHAWLGSTTVALVVLQPLTLAGSHDTYINGQMWDYMTSQENFDR 183
Db 145 VCHPITSLRRNNAKAYVICALVMSVTLCLVFNLIFFVSPKVNICTHTTPEDFAR 204

Oy 184 LFAY--GIVLTLSGF--LSLLGHFGVLFTDQGEPPDQARGEHEDRQHSQVHDPHTGV 239
```

Db 205 YVEYSTAIMCLLFGIPCLLIAGCYGLMTRMLKPIVS-----GNQOTLPSYKRSIKT-- 257  
 Qy 240 WPLHPLFCALPHSLPHLLPHLLSAGSLPALDGSQC-----GLQDMEASGECEQ 288  
 Db 258 ----IIFWIAFAICFMPFHITRTLYYYARLLGIKCYALNVINVTYKTRPLASANSC-- 311  
 Qy 289 LPQSPSPVLSF-KGGKNRVLLQKLRQNLGEPHAGKRCPCGLN 330  
 Db 312 ---IDPILYFLANDRYRRRLRTVRRS-----SVNRRCMHTN 347

## RESULT 7

ID Q4SELS\_TETNG PRELIMINARY; PRT; 310 AA.  
 AC Q4SELS;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE Chromosome 10 SCAP14616, whole genome shotgun sequence.  
 DE (Fragment)  
 GN ORFNames=GSTENG00019499001;

OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
 RA Bienmont C., Skalli Z., Cattellico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin V., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,  
 RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 RT the early vertebrate proto-karyotype."  
 RL Nature 431:946-957(2004).  
 RN [2]

RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; CAAE01014616; GACG00917.1; -; Genomic\_DNA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR002286; P2\_purnoceptor.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PRINTS; PR01157; P2YPURNOCTR.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; UNKNOWN\_1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.  
 FT NON\_TER 1  
 FT NON\_TER 310 310  
 SQ SEQUENCE 310 AA; 35979 MW; DC6DF8ADB949D176 CRC64;

Query Match 23.2%; Score 420.5; DB 2; Length 310;  
 Best Local Similarity 34.1%; Pred. No. 5.2e-23;  
 Matches 109; Conservative 52; Mismatches 122; Indels 37; Gaps 10;  
 Qy 15 CQFSEKYQVLSLAYSIIIFILGLPLNGTVLHFHFGQTKRSCATTYLVNVLADLVYL 74  
 Db 3 CKFKEDFKVILLPVSYALVFVFLGLNGLALVIVFRTKAWKPSVTVMFNLTMCDTLYL 62

Qy 75 -LPFLITYSDDRWPFGECLLKVHFLFYINLYGSIILLTCTISVHOFGLVCHPLCSLPY 133  
 Db 63 TLPLIYYADENWPFSEPKIIRLFYANLYGSIILFCCISLHRIGVCYPRSYLW 122  
 Qy 134 RTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTQENFDRLFAYGIVLTL 193  
 Db 123 LSARRAKFISVAVWVLSQSPVLYFSRIRKDKSSRICYDTTSPLEFDDFLVYSSVISV 182  
 Qy 194 SGFLSLGHFGVLFDTG-----QEPQARG--EPHEDRQHSPOVHPDHTGWP 241  
 Db 183 LMF--ALPFMTVMVCMGLMVKLLLEVSRGAKGNLSAROSKQSKVMIIIVLATF--- 237  
 Qy 242 LHPLFCALPHSLPHLLPHLLSAGSLPALDGSQ--CGLQDMEASGECEQLPOP----- 292  
 Db 238 ---MLCFLPFH--LTRSLYYSFRIQVNPHQITCGM--LEAINVAVKTRPLASANSC 289  
 Qy 293 -SPVLSFKGKN-RVRLQK 310  
 Db 290 LDPILYFLAGQDIRSNLTKK 309

## RESULT 8

OSBJ79\_XENTR PRELIMINARY; PRT; 543 AA.  
 AC OSBJ79;  
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

DE Hypothetical protein.  
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodidae; Xenopus; Silurana.  
 OX NCBI\_TaxID=8364;  
 RN [1]

## NUCLEOTIDE SEQUENCE.

RP TISSUE=Embryo;  
 RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

## NUCLEOTIDE SEQUENCE.

RP TISSUE=Embryo;  
 RC Klein S., Gerhard D.S.; to the EMBL/GenBank/DBJ databases.  
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
 DR EMBL; BC091589; AAH91589.1; -; mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-..; IEA.  
 DR GO; GO:004872; F:receptor activity; IEA.  
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.  
 DR GO; GO:0007165; P:signal transduction; IEA.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR002286; P2\_purnoceptor.





```

CC  -!- FUNCTION: Receptor for extracellular UTP > ADP = 2-methylthio-ATP
CC  > ADP-beta-S > ATP = ATP-gamma-S. The activity of this receptor is
CC  mediated by G proteins which activate a phosphatidylinositol-
CC  calcium second messenger system. Functionally coupled to
CC  phospholipase C.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- TISSUE SPECIFICITY: Abundantly expressed in various tissues
CC  including lung, stomach, intestine, spleen, mesentery, heart, and,
CC  most prominently, aorta.
CC  -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
CC  EMBL; D63665; BAA09816.1; -; mRNA.
CC  EMBL; BC072520; AAH72520.1; -; mRNA.
CC  DR  PIR; I55450; I55450.
CC  DR  HSSP; P34996; 1DDO.
CC  DR  Ensembl; ENSRNOG0000019270; Rattus norvegicus.
CC  DR  RGD; 620269; P2ry6.
CC  DR  GO; GO:0016324; C:apical plasma membrane; IDA.
CC  DR  GO; GO:0016323; C:basolateral plasma membrane; IDA.
CC  DR  InterPro; IPR000276; GPCR_Rhodpsn.
CC  DR  InterPro; IPR002286; P2_purinocptor.
CC  DR  InterPro; IPR001973; P2y6_purinocptor.
CC  DR  Pfam; PF00001; 7tm 1; 1.
CC  DR  PRINTS; PR00237; GPCRHHODPSN.
CC  DR  PRINTS; PR01068; P2Y6PRNOCPTR.
CC  DR  PRINTS; PR01157; P2Y6PRNOCPTR.
CC  DR  PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
CC  DR  PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
CC  KW  G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
CC  Transmembrane.
CC  FT  TOPO_DOM 1 27 Extracellular (Potential).
CC  FT  TRANSMEM 28; 48 1 (Potential).
CC  FT  TOPO_DOM 49 62 Cytoplasmic (Potential).
CC  FT  TRANSMEM 63 83 2 (Potential).
CC  FT  TOPO_DOM 84 101 Extracellular (Potential).
CC  FT  TRANSMEM 102 122 3 (Potential).
CC  FT  TOPO_DOM 123 144 Cytoplasmic (Potential).
CC  FT  TRANSMEM 145 165 4 (Potential).
CC  FT  TOPO_DOM 166 194 Extracellular (Potential).
CC  FT  TRANSMEM 195 215 5 (Potential).
CC  FT  TOPO_DOM 216 236 Cytoplasmic (Potential).
CC  FT  TRANSMEM 237 257 6 (Potential).
CC  FT  TOPO_DOM 258 280 Extracellular (Potential).
CC  FT  TRANSMEM 281 303 7 (Potential).
CC  FT  TOPO_DOM 304 328 Extracellular (Potential).
CC  FT  CARBOHYD 5 N-linked (GlcNAc...) (Potential).
CC  FT  CARBOHYD 5 N-linked (GlcNAc...) (Potential).
CC  FT  DISULFID 173 173 By similarity.
CC  SQ  SEQUENCE 328 AA; 36677 MW; 58BEE1997038BA5B CRC64;
CC  Query Match 22.2%; Score 402; DB 1; Length 328;
CC  Best Local Similarity 32.5%; Pred. No. 1.3e-21;
CC  Matches 108; Conservative 53; Mismatches 137; Indels 34; Gaps 9;
CC  QY 1 MEKVDMNTSQEGL----CFSEKTKQVYLSLAYSIIFLGLPLNGTVMWHFWGQTKRWS 56
CC  Db 1 MER-DNGTIQAPGLPTTCVYREDPFRLLPPVYSVVLVGLPLNVCVIAQICASRRILT 59
CC  QY 57 CATTYLVNLMVADLLYL-LPFLIITYISLDDRPFGELCKLVHFLYINLYSGILLTLC 115
CC  Db 60 RSAVYTLNLADLLVACSLPLLIYNYARGDHWPFGLACRLVFLFVYANLHGSILFTLC 119
CC  QY 116 ISVHQLGVCHPLCSLPR-TRHAWLGTSTTVALVVLQLLPTLAFSTHDYINGOMIYWD 174
CC  Db 120 ISFYGLGICHPLAPWHKRGGRRAAWGVGVVVLVVTQAQCLPTAVFAATGIQRNRTCYD 179
CC  QY 175 MTSQENFDRFLPAYGIVLTLISGFL----SLLGHFGVLFTDQGEPPDQARGEPHEDRQHSFQ 230

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Db 180 LSPPTLSRYLPYGNWALTVIGFLPFTALLACYCRMARRLCRQDGPAGFVAQERSKAAR 239
QY 231 VHPDPTGVWPLHPLFCALPHSHLLPHLLI-SAFSGLPALDGSOGCLQDWEASCECQL 289
Db 240 M-----AVVAAVVISFLPFHTTKTAYLAVRSTPGVSCPVLTFFAAYKQTR 287
QY 290 PQPS-----PVLSPF---KGGKRVRLQL 311
Db 288 PFASANSVLDILPFYFTQCKFRQPHDLQL 319

RESULT 11
P2RY6 MOUSE
ID P2RY6 MOUSE STANDARD; PRT; 328 AA.
AC Q9ERK3;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE P2Y purinoceptor 6 (p2y6).
GN Name=P2ry6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/SVEV;
RX MEDLINE=21160552; PubMed=11259526;
RA Lazarowski E.R., Rochelle L.G., O'Neal W.K., Ribeiro C.M.P.,
RA Grubb B.R., Zhang V., Harden T.K., Boucher R.C.;
RT "Cloning and functional characterization of two murine uridine
RT nucleotide receptors reveal a potential target for correcting ion
RT transport deficiency in cystic fibrosis gallbladder.";
RL J. Pharmacol. Exp. Ther. 297:43-49 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Receptor for extracellular UTP > ADP = 2-methylthio-ATP
CC > ADP-beta-S > ATP = ATP-gamma-S. The activity of this receptor is
CC mediated by G proteins which activate a phosphatidylinositol-
CC calcium second messenger system. Functionally coupled to
CC phospholipase C (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

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EMBL; AF298899; AAC24619.1; -, Genomic_DNA.
DR DT
EMBL; BC027331; AAH27331.1; -, mRNA.
DR DT
EMBL; BC064095; AAH64095.1; -, mRNA.
DR DT
Ensembl; ENSMUSG00000048779; Mus musculus.
DR DT
MGI; MGI:2673874; P2ry6.
DR DT
GO; GO:0016021; C:integral to membrane; TAS.
DR DT
GO; GO:0019103; F:pyrimidine nucleotide binding; IC.
DR DT
GO; GO:0045029; F:UDP-activated nucleotide receptor activity; IDA.
DR DT
GO; GO:0030321; P:transmembrane chloride transport; IDA.
DR DT
InterPro; IPR000276; GPCR_Rhodpsn.
DR DT
InterPro; IPR002286; P2_purnocptor.
DR DT
InterPro; IPR001973; P2Y6_purnocptor.
DR DT
Pfam; PF00001; 7tm_1; 1.
DR DT
PRINTS; PR00237; GPCRHHODOPSN.
DR DT
PRINTS; PR01068; P2Y6PRNOCPT.
DR DT
PRINTS; PR01157; P2Y6PRNOCPT.
DR DT
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
DR DT
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR DT
G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
KW Transmembrane.
FT TOPO_DOM 1 27 Extracellular (Potential).
FT TRANSMEM 28 48 1 (Potential).
FT TOPO_DOM 49 62 Cytoplasmic (Potential).
FT TRANSMEM 63 83 2 (Potential).
FT TOPO_DOM 84 101 Extracellular (Potential).
FT TRANSMEM 102 122 3 (Potential).
FT TOPO_DOM 123 144 Cytoplasmic (Potential).
FT TRANSMEM 145 165 4 (Potential).
FT TOPO_DOM 166 194 Extracellular (Potential).
FT TRANSMEM 195 215 5 (Potential).
FT TOPO_DOM 216 236 Cytoplasmic (Potential).
FT TRANSMEM 237 257 6 (Potential).
FT TOPO_DOM 258 280 Extracellular (Potential).
FT TRANSMEM 281 303 7 (Potential).
FT TOPO_DOM 304 328 Extracellular (Potential).
FT CARBOHYD 5 N-linked (GlcNAc...) (Potential).
FT DISULFID 173 173 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 328 AA; 36721 MW; 00F9DF5ADADF903E CRC64;

Query Match
Best Local Similarity 21.9%; Score 397; DB 1; Length 328;
Matches 106; Conservative 55; Mismatches 137; Indels 34; Gaps 9;

Qy 1 MEKVDNMTSBOQGL-----CQSEKVKQVYLSLAYSIIFILGLPLNGTVLWHPWGQTKRWS 56
Db 1 MEQ-DNGTIQAPGLPPTTCVYREDPKRLLLTPVYVVLVWGLPLNICVIAQICASRRLLT 59

Qy 57 CATTYLVNLMVADLLYL-LPFLIITYSLDRWPFGEILLCKLVHFLFYINLYGSIILLTLC 115
Db 60 RSAYVTLNLALADLMYACSLPLLYNYARGDHPFPGDLACRFVRFLEYANLHLSILFLTC 119

Qy 116 ISVHQFLGVCHPLCSLPYR-TRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 174
Db 120 ISFORYLIGICHLASWHKGRRAAWVCGVVLAVTAQCLPTAVFATGQRNRTVCYD 179

Qy 175 MTSQENFDRLPAYGIVLTLSGFL-----SLLGHFGLVFTDGOEPDQARGEHPHQSPSQ 230
Db 180 LSPPILSTRYLPYGMALTVIGFLFPFALLACACRMARRLCQDGPAGPVAQERRSKAAR 239

Qy 231 VHPDPTGVWPLHPLFCALPHSLLPHLL-SAFSGLPALDGGSCQLQDMWASGEQQL 289
Db 240 M-----AVVAAVFAISLPLFPHTTKTAYLAVRSTPGVSCFVLETFAAAYKQTR 287

Qy 290 PQPS-----PVLGF-----KGGKRVRLLOKL 311
Db 288 PFASVNSVLDFILFYFTQCKFRQPHDLLQL 319

RESULT 12
P2RY4_RAT
ID P2RY4_RAT STANDARD; PRT; 361 AA.

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O35811;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
P2Y purinocceptor 4 (P2Y4).
Name=P2RY4; Synonyms=P2Y4;
Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RA Bogdanov Y.D., Wildman S., King B.F., Burnstock G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
[2]
NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98421785; Pubmed=9751165;
RA Webb T.E., Henderson D., Roberts J.A., Barnard E.A.;
RT "Molecular cloning and characterization of the rat P2Y4 receptor.";
J. Neurochem. 71:1348-1357(1998).
CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that
activate a phosphatidylinositol-calcium second messenger system.
CC Not activated by ADP or UDP.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Widely expressed at low levels. In brain,
higher expression in the pineal gland and ventricular system.
CC -!- PM: Phosphorylation of Ser-329 and Ser-330 is a key step in
agonist-dependent desensitization and loss of surface P2RY4. This
phosphorylation does not involve PKC, nor other calcium-activated
kinases (By similarity).
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
-----
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removed.
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EMBL; Y14705; CAA75007.1; -, Genomic_DNA.
EMBL; Y11433; CAA72241.1; -, mRNA.
DR DT
HSP; P34996; IDDD.
DR DT
Ensembl; ENSRNOG00000002953; Rattus norvegicus.
DR DT
RGD; 61798; P2RY4.
DR DT
GO; GO:0016324; C:apical plasma membrane; IDA.
DR DT
GO; GO:0016323; C:basolateral plasma membrane; IDA.
DR DT
GO; GO:0005524; F:ATP binding; IDA.
DR DT
InterPro; IPR000276; GPCR_Rhodpsn.
DR DT
InterPro; IPR002286; P2_purnocptor.
DR DT
InterPro; IPR000018; P2Y4_purnocptor.
DR DT
Pfam; PF00001; 7tm_1; 1.
DR DT
PRINTS; PR00237; GPCRHHODOPSN.
DR DT
PRINTS; PR01066; P2Y6PRNOCPT.
DR DT
PRINTS; PR01157; P2Y6PRNOCPT.
DR DT
PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR DT
PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
DR DT
G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
Transducer; Transmembrane.
FT TOPO_DOM 1 30 Extracellular (Potential).
FT TRANSMEM 31 58 1 (Potential).
FT TOPO_DOM 59 68 Cytoplasmic (Potential).
FT TRANSMEM 69 91 2 (Potential).
FT TOPO_DOM 92 108 Extracellular (Potential).
FT TRANSMEM 109 127 3 (Potential).
FT TOPO_DOM 128 149 Cytoplasmic (Potential).
FT TRANSMEM 150 170 4 (Potential).
FT TOPO_DOM 171 192 Extracellular (Potential).
FT TRANSMEM 193 218 5 (Potential).
FT TOPO_DOM 219 242 Cytoplasmic (Potential).
FT TRANSMEM 243 265 6 (Potential).
FT TOPO_DOM 266 283 Extracellular (Potential).

```



[4]  
 NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RP TISSUE=Kidney, and Leukocyte;  
 RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RX Strausberg R.L., Fellings E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huily S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J.J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -!- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that  
 CC activate a phosphatidylinositol-calcium second messenger system.  
 CC The affinity range is UTP = ATP > ATP-gamma-S >> 2-methylthio-ATP  
 CC = ADP.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- TISSUE SPECIFICITY: Spleen, testis, kidney, liver, lung, heart and  
 CC brain.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC  
 CC EMBL; U07225; AAC04923.1; -; mRNA.  
 CC EMBL; AY136753; AA01279.1; -; mRNA.  
 CC EMBL; BC012104; AA012104.1; -; mRNA.  
 CC EMBL; BC028135; AA028135.1; -; mRNA.  
 CC HSSP; P34996; 1DD0.  
 CC Ensembl; ENSG00000175591; Homo sapiens.  
 CC HGNC; HGNC:8541; P2RY2.  
 CC H-InvDB; HIX0009916; -.  
 CC MIM; 600041; -.  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004872; F:receptor activity; TAS.  
 CC GO; GO:0006873; P:cell ion homeostasis; TAS.  
 CC GO; GO:0007200; P:G-protein signaling, coupled to IP3 second . . .; TAS.  
 CC InterPro; IPR002276; GPCR\_Rhodopsn.  
 CC InterPro; IPR002286; P2\_purinocptor.  
 CC InterPro; IPR003356; P2\_purinocptor.  
 CC Pfam; PF00001; 7tm\_1; 1.  
 CC PRINTS; PR00237; GPCR\_Rhodopsn.  
 CC PRINTS; PR00594; P2Y2\_PURNOCPTOR.  
 CC PRINTS; PR01157; P2Y\_PURNOCPTOR.  
 CC PROSITE; PS00237; G\_PROTEIN\_RECP\_F1\_1; 1.  
 CC PROSITE; PS00262; G\_PROTEIN\_RECP\_F1\_2; 1.  
 CC G-protein coupled receptor; Glycoprotein; Receptor; Transducer;  
 KW Transmembrane.  
 KW TOPO\_DOM 1 32 Extracellular (Potential).  
 FT TRANSMEM 33 59 1 (Potential).  
 FT TOPO\_DOM 60 70 Cytoplasmic (Potential).  
 FT TRANSMEM 71 93 2 (Potential).  
 FT TOPO\_DOM 94 110 Extracellular (Potential).  
 FT TRANSMEM 111 129 3 (Potential).  
 FT TOPO\_DOM 130 152 Cytoplasmic (Potential).  
 FT TRANSMEM 153 172 4 (Potential).  
 FT TOPO\_DOM 173 194 Extracellular (Potential).  
 FT TRANSMEM 195 220 5 (Potential).

FT TOPO\_DOM 221 246 Cytoplasmic (Potential).  
 FT TRANSMEM 247 269 6 (Potential).  
 FT TOPO\_DOM 270 287 Extracellular (Potential).  
 FT TRANSMEM 288 309 7 (Potential).  
 FT TOPO\_DOM 310 377 Cytoplasmic (Potential).  
 FT CARBOHYD 9 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 13 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 106 183 By similarity.  
 FT CONFLICT 312 R -> S (in Ref. 4; AA012104).  
 FT CONFLICT 350 E -> G (in Ref. 1).  
 FT CONFLICT 359 S -> F (in Ref. 1).  
 SQ SEQUENCE 377 AA; 42290 MW; EE557A857A269AC6 CRC64;  
 Query Match. 21.8%; Score 395.5; DB 1; Length 377;  
 Best Local Similarity 33.0%; Pred. No. 4.4e-21;  
 Matches 118; Conservative 41; Mismatches 118; Indels 81; Gaps 13;  
 QY 15 CQSEKYQVYLSLAYSIIFILGLPLNGTGLVHFWGOTKEWSCATTLYLVNLMVADLLYLVL 74  
 Db 25 CRNEDPKYLLPVSYGVGVCVGLCLNVALYIFLCRLKTNASTTTFHFLAVSDALYAA 84  
 QY 75 -LPFLIITYSLDRWPFGELLKLVHFLFYINLYGSIILLETICISVHOFGLGVCHPLCLSPY 133  
 Db 85 SLPLLVYYARGDHPFPSTVLCKLVRLFYTNLYCSILFLTCSVHRCLGVRLRLSLRW 144  
 QY 134 RTRRHAWLGSTTVALVQLLPTLAPSHDYINGQMIWYDMSQENFDRLFAYGIVLTL 193  
 Db 145 GRARYARRVAGAVVWLACQAPVLYFVTTSARGRVTCHTDTSAPELFSFVAYSSVM-- 202  
 QY 194 SGFLSLHGFGVLF-----TDGQEPDQARGEPHEDRQHSQVHP 233  
 Db 203 ---LGLL--FAVPFAVILVCVLMARLLKPAVGTSG-----GLPRAKKSVRT-- 246  
 QY 234 DHPTGVWPLPLF--CALPYH-----SLLLPHLLSAFS-----GLPALDGSQCG 276  
 Db 247 -----IAVLAVPALCFLEPHVTTLTYSPSLDLSCHTLNAINMAYKVRPLASANS- 300  
 QY 277 LQDMEASGECEQLPQSPSVLSFKGKRVRLLOKLRQNLKGEHPA--GRKRCPCGLNRS 332  
 Db 301 -----LDPVLYFLAGQLRVFARDAKP-PTGSPSPATPARRRL-GLRRS 341  
 RESULT 15  
 P2RY4\_MOUSE  
 ID P2RY4\_MOUSE STANDARD; PRT; 361 AA.  
 AC Q9JJS7;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE P2Y purinocceptor 4 (P2Y4).  
 GN Name=P2RY4; Synonyms=P2y4r;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=129/SWJ;  
 RX MEDLINE=21185993; PubMed=11290369; DOI=10.1016/S0014-2999(01)00875-5;  
 RA Suarez-Huerta N., Pouillon V., Boeynaems J.-M., Robaye B.;  
 RT "Molecular cloning and characterization of the mouse P2Y4 nucleotide  
 RT receptor.";  
 RL Eur. J. Pharmacol. 416:197-202(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 RC STRAIN=C57BL/6J; Tissue=Skin;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
Dalla E., Dragapi T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,  
Grimmond S., Gustinch S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
Maglott D.R., Maitais L., Marchionni L., McKenzie L., Miki H.,  
Nagashima T., Nomata K., Okido T., Pavan W.J., Partea G., Pesole G.,  
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,  
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,  
Wilming L.G., Wynshaw-Boris A., Yangisawa M., Yang I., Yang L.,  
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
Birney E., Hayashizaki Y.;  
"Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs";  
Nature 420:563-573(2002).  
CC -1- FUNCTION: Receptor for ATP and UTP coupled to G-proteins that  
activate a phosphatidylinositol-calcium second messenger system.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- TISSUE SPECIFICITY: Expressed in the liver, intestine, stomach,  
bladder and lung.  
CC -1- PM: Phosphorylation of Ser-329 and Ser-330 is a key step in  
agonist-dependent desensitization and loss of surface P2RY4. This  
phosphorylation does not involve PKC, nor other calcium-activated  
kinases (By similarity).  
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
-----  
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the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
-----  
CC EMBL: AJ277752; CAB91043.1; -; Genomic\_DNA.  
CC EMBL: AK076364; BAC36314.1; -; mRNA.  
CC HSPSP; P34996, 1DDX.  
CC Ensembl: ENSMUSG0000044359; Mus musculus.  
CC MGI: MGI:1926594; P2ry4.  
CC GO: GO:016021; C:integral to membrane; TAS.  
CC GO: GO:0019103; F:pyrimidine nucleotide binding; IC.  
CC GO: GO:0045030; F:UTP-activated nucleotide receptor activity; IDA.  
CC GO: GO:0030321; P:transpore nucleotide chloride transport; IDA.  
CC InterPro: IPR000276; GPCR\_Rhodopsn.  
CC InterPro: IPR002286; P2\_purinocptor.  
CC InterPro: IPR000018; P2y4\_purinocptor.  
CC Pfam: PF00001; 7tm\_1; 1.  
CC PRINTS: PR00237; GPCR\_Rhodopsn.  
CC PRINTS: PR01066; P2y4PRNOCPTR.  
CC PRINTS: PR01157; P2yPURNOCPTR.  
CC PROSITE: PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
CC PROSITE: PS00262; G\_PROTEIN\_RECEP\_F2\_1.  
CC G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;  
Transducer; Transmembrane.  
CC TOPO\_DOM 1 30 Extracellular (Potential).  
CC TRANSFM 31 58 1 (Potential).  
CC TOPO\_DOM 59 68 Cytoplasmic (Potential).  
CC TRANSFM 69 91 2 (Potential).  
CC TOPO\_DOM 92 108 Extracellular (Potential).  
CC TRANSFM 109 127 3 (Potential).  
CC TOPO\_DOM 128 149 Cytoplasmic (Potential).  
CC TRANSFM 150 170 4 (Potential).  
CC TOPO\_DOM 171 192 Extracellular (Potential).  
CC TRANSFM 193 218 5 (Potential).  
CC TOPO\_DOM 219 242 Cytoplasmic (Potential).  
CC TRANSFM 243 265 6 (Potential).

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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:35:04 ; Search time 186 Seconds  
(without alignments)  
786.630 Million cell updates/sec

Title: US-10-088-726-20  
Perfect score: 1812  
Sequence: 1 MEKVDMTSQGLQCFSEK.....NKLGEHPAGRKRCPLNRSQ 333

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 21:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1812	100.0	333	4	AAG64125 Human G p
2	1804	99.6	361	7	AB99264 Human P2Y
3	1798	99.2	360	5	AB998145 Human GPC
4	1536	84.8	295	5	AAU11251 Human P2Y
5	1397	77.1	361	5	AD116630 Human NOV
6	1387	76.5	361	8	ADN42284 Human nov
7	1051	58.0	338	7	ADC26009 Human pur
8	1051	58.0	338	7	ABW00804 Human GPC
9	1047	57.8	339	5	AB98146 Human GPC
10	1047	57.8	339	5	AAE18640 Human G-p
11	1047	57.8	339	8	ADQ30394 Human GPC
12	1041	57.5	338	7	ADC26000 Human pur
13	936	51.7	271	7	ADC86167 Human GPC
14	921	50.8	170	4	AG808935 Human nGP
15	921	50.8	170	5	ABG93753 Human G p
16	779	43.0	302	8	ADQ30396 Mouse GPC
17	449	24.8	328	5	AD116984 NOVX prot
18	449	24.8	328	5	AD116983 NOVX prot
19	449	24.8	328	8	ADP49191 Chick P2Y
20	429	23.7	374	4	ADR89634 Chick P2Y
21	429	23.7	374	5	AAE04390 Turkey NO
22	429	23.7	374	5	AD116982 Turkey P2
23	429	23.7	374	8	ADR89631 Turkey G-
24	424	23.4	537	5	AAU74538 Human P2Y

25	424	23.4	537	5	AD116981	Adil16981 Human NOV
26	424	23.4	537	8	ADR89632	Adr89632 Xenopus P
27	402.5	22.2	377	4	AAE01144	Aae01144 Human pur
28	402	22.2	328	7	ADD45304	Add45304 Rat Prote
29	397	21.9	328	2	AAR91224	Aar91224 Mouse pan
30	397	21.9	328	7	ADC37339	Adc37339 Nuclear f
31	397	21.9	328	8	ADO29601	Ado29601 Mouse GPC
32	396	21.9	361	5	AD116985	Adil16985 Rat NOVX
33	396	21.9	361	7	ADH69290	Adh69290 Rat orpha
34	396	21.9	361	8	ADF91782	Adf91782 Rat orpha
35	396	21.9	361	8	ADR89629	Adr89629 Rat G-pro
36	396	21.9	361	8	ADS84264	Ads84264 Rat G pro
37	395.5	21.8	377	4	AAE01143	Aae01143 Human pur
38	395.5	21.8	377	6	AAE04392	Aae04392 Human P2-
39	395.5	21.8	377	6	ABP81866	Abp81866 Human pur
40	395.5	21.8	377	7	ADe62766	Ade62766 Human Pro
41	395.5	21.8	377	8	ADO29596	Ado29596 Human GPC
42	395.5	21.8	377	8	ADP49189	Adp49189 Human P2Y
43	394.5	21.8	328	2	AAR91225	Aar91225 Human pla
44	394	21.7	361	8	ADO29599	Ado29599 Mouse GPC
45	389.5	21.5	328	4	AAE04393	Aae04393 Human P2-

ALIGNMENTS

RESULT 1  
AAG64125  
ID AAG64125 standard; protein; 333 AA.  
XX  
AC AAG64125;  
XX  
DT 25-SEP-2001 (first entry)  
XX  
DE Human G protein-coupled receptor GPRV71.  
XX  
KW Human; guanosine triphosphate binding protein-coupled receptor;  
KW G protein-coupled receptor; GPRV8; GPRV12; GPRV16; GPRV21; GPRV40;  
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;  
KW Alzheimer's disease; cytostatic; hepatotropic; nootropic;  
KW neuroprotective; gene therapy; peptide therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200148188-A1.  
XX  
PD 05-JUL-2001.  
XX  
PF 28-DEC-2000; 2000WO-JP009408.  
XX  
PR 28-DEC-1999; 95JP-00375152.  
PR 31-MAR-2000; 2000JP-00101339.  
XX  
(HELI-) HELIX RES INST.  
PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;  
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;  
DR WPI; 2001-425662/45.  
XX N-PSDB; AAH73516.  
XX  
PT New DNA encoding guanosine triphosphate binding protein coupled receptors  
PT and their expression products for screening potential anticancer and  
PT nootropic drugs and in diagnosis of these diseases.  
XX  
PS Example 1; Page 132-135; 170pp; Japanese.  
XX  
CC The invention relates to nine human guanosine triphosphate binding  
CC protein (G protein)-coupled receptors designated GPRV8, GPRV12, GPRV16,  
CC GPRV21, GPRV40, GPRV47, GPRV51, GPRV71 and GPRV72, and to the genes  
CC encoding them. These genes and proteins and antibodies against the  
CC protein are useful in the treatment, prevention, diagnosis and  
CC investigation of diseases associated with G protein-coupled receptors,

CC including cancer, cirrhosis of the liver and Alzheimer's disease. The  
 CC present sequence is a G protein-coupled receptor of the invention  
 SQ Sequence 333 AA;

Query Match 100.0%; Score 1812; DB 4; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 7.4e-191;  
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKVDWNTSQEQGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSATT 60  
 DB 1 MEKVDWNTSQEQGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSATT 60

QY 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGEELCKLVHFLFYINLYGSILLTTCISVHQ 120  
 DB 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGEELCKLVHFLFYINLYGSILLTTCISVHQ 120

QY 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 180  
 DB 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 180

QY 181 FDLRFAYGIVLTLSGFLSLGLHFGVLTDCQEPDQARGEPEHEDRQHSFSPQVHPDHPGTVW 240  
 DB 181 FDLRFAYGIVLTLSGFLSLGLHFGVLTDCQEPDQARGEPEHEDRQHSFSPQVHPDHPGTVW 240

QY 241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQLPQSPVLSFKG 300  
 DB 241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQLPQSPVLSFKG 300

QY 301 GKNRVLLQKLQKRLQKLGHPAGRCPCGLNRSG 333  
 DB 301 GKNRVLLQKLQKRLQKLGHPAGRCPCGLNRSG 333

RESULT 2  
 ADB99264  
 ID ADB99264 standard; protein; 361 AA.  
 XX AC ADB99264;  
 XX DT 04-DEC-2003 (first entry)  
 XX DE Human p2Y2li protein.  
 XX KW gene; human; P2Y2li; chromosome 3; G protein-coupled receptor; GPCR;  
 XX KW Class A rhodopsin-like sub-family; gene therapy; receptor.  
 XX OS Homo sapiens.  
 XX PN DE10144044-A1.  
 XX PD 27-MAR-2003.  
 XX PF 07-SEP-2001; 2001DE-01044044.  
 XX PR 07-SEP-2001; 2001DE-01044044.  
 XX PA (BRUE/) BRUESS M.  
 XX PA (BOEN/) BOENISCH H.  
 XX PA (VKUE/) VON KUEGELGEN I.  
 XX PI Bruess M, Boenisch H, Von Kuegelgen I;  
 XX WPI; 2003-364675/35.  
 XX DR N-PSDB; ADB99267.  
 XX PT New human gene p2Y2li and encoded G protein-coupled receptor, useful for  
 XX treatment and diagnosis of receptor-associated diseases and for drug  
 XX screening.  
 XX PS Disclosure; Page 4; 6pp; German.  
 XX CC This invention describes the human p2Y2li gene and its 5'- and 3'-

CC untranslated regions, located on chromosome 3 which is a novel G protein-  
 CC coupled receptor (GPCR). The protein encoded by P2Y2li is expressed in  
 CC blood cells, testis and embryonal kidney cells and contains potential  
 CC sites for phosphorylation by protein kinase C and casein kinase II. It is  
 CC a member of the Class A rhodopsin-like sub-family of G protein-coupled  
 CC receptors and it probably a nucleoside/nucleotide receptor that mediates  
 CC action of nucleosides/nucleotides or their sugar derivatives. P2Y2li and  
 CC antibodies directed against the encoded protein are useful in diagnosis  
 CC and treatment (including gene therapy) of diseases associated with  
 CC abnormal levels of P2Y2li expression, in screening assays for modulators,  
 CC potential therapeutic agents, and to produce transgenic animals, e.g. for  
 CC identifying diseases associated with abnormal expression of P2Y2li. This  
 CC sequence represents the human P2Y2li protein described in the disclosure  
 XX of the invention.  
 SQ Sequence 361 AA;

Query Match 99.6%; Score 1804; DB 7; Length 361;  
 Best Local Similarity 99.7%; Pred. No. 6.3e-190;  
 Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MEKVDWNTSQEQGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSATT 60  
 DB 29 MEKVDWNTSQEQGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSATT 88

QY 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGEELCKLVHFLFYINLYGSILLTTCISVHQ 120  
 DB 89 YLVNLMVADLLYVLLPFLIITYSLDDRPFGEELCKLVHFLFYINLYGSILLTTCISVHQ 148

QY 121 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 180  
 DB 149 FLGVCHPLCSLPYRTRRHAWLGTSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208

QY 181 FDLRFAYGIVLTLSGFLSLGLHFGVLTDCQEPDQARGEPEHEDRQHSFSPQVHPDHPGTVW 240  
 DB 209 FDLRFAYGIVLTLSGFLSLGLHFGVLTDCQEPDQARGEPEHEDRQHSFSPQVHPDHPGTVW 268

QY 241 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQLPQSPVLSFKG 300  
 DB 269 PLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQDMEASGECEQLPQSPVLSFKG 328

QY 301 GKNRVLLQKLQKRLQKLGHPAGRCPCGLNRSG 333  
 DB 329 GKNRVLLQKLQKRLQKLGHPAGRCPCGLNRSG 361

RESULT 3  
 ABB98145  
 ID ABB98145 standard; protein; 360 AA.  
 XX AC ABB98145;  
 XX DT 17-OCT-2002 (first entry)  
 XX DE Human GPCR designated PFI-020.  
 XX KW Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;  
 XX KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;  
 XX KW disorder; PFI-020.  
 XX OS Homo sapiens.  
 XX PN EP1215214-A1.  
 XX PD 19-JUN-2002.  
 XX PF 04-DEC-2001; 2001EP-00310137.  
 XX PR 18-DEC-2000; 2000GB-00030855.  
 XX PR 17-JAN-2001; 2001GB-00001222.  
 XX PA (PFIZ ) PFIZER LTD.  
 XX PA (PFIZ ) PFIZER INC.

XX Fiddock MD;  
 XX WPI; 2002-510798/55.  
 DR N-PSDB; ABQ76000.  
 XX  
 DR New polynucleotide encoding G protein-coupled receptor PFI-020, useful  
 PT e.g. for treating eating and sleeping disorders and for identifying  
 PT specific modulators.  
 XX  
 XX Claim 1 (a); Page 11-12; 23pp; English.  
 PS  
 XX The invention relates to an isolated polynucleotide encoding a novel  
 CC polypeptide belonging to the class of proteins known as G-protein coupled  
 CC receptors (GPCRs). The activity of proteins of the invention may be  
 CC described as, antidepressant and neuroleptic. Polynucleotides of the  
 CC invention are used for recombinant expression of the G protein-coupled  
 CC receptor (PFI-020) polypeptides, to create transgenic animals, as source  
 CC of primers, probes, antisense sequences and ribozymes and in gene  
 CC therapy. Therapeutic agents of the invention can be used to treat a wide  
 CC range of disorders, particularly mood disorders, depression or arousal,  
 CC especially eating and sleeping disorders. The current sequence represents  
 CC a human GPCR designated PFI-020  
 XX  
 XX Sequence 360 AA;  
 SQ  
 Query Match 99.2%; Score 1798; DB 5; Length 360;  
 Best Local Similarity 99.7%; Pred. No. 2.9e-189;  
 Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MEKVDNMTSQBGLCFQSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60  
 DB 29 MEKVDNMTSQBGLCFQSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 88  
 QY 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLCKLVHFLFYINLYGSILLTLCISVHQ 120  
 DB 89 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLCKLVHFLFYINLYGSILLTLCISVHQ 148  
 QY 121 FLGVCHPLCSLPYRTRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 180  
 DB 149 FLGVCHPLCSLPYRTRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 208  
 QY 181 FDRLPAYGIVLTLGSLGFLHGFVLTGQEPDQARGEPHEDROHSPQVHPDPTGVW 240  
 DB 209 FDRLPAYGIVLTLGSLGFLHGFVLTGQEPDQARGEPHEDROHSPQVHPDPTGVW 268  
 QY 241 PLHPLFCALPYHSLLLPHLLSAFSLGSLPALDGSQGLQDMASGCEQLPQSPVLSFKG 300  
 DB 269 PLHPLFCALPYHSLLLPHLLSAFSLGSLPALDGSQGLQDMASGCEQLPQSPVLSFKG 328  
 QY 301 GKNRVLLQKLRQNKLGHPAGRCPCGLNRS 332  
 DB 329 GKNRVLLQKLRQNKLGHPAGRCPCGLNRS 360  
 RESULT 4  
 AAU11251  
 ID AAU11251 standard; protein; 295 AA.  
 XX  
 AC AAU11251;  
 XX  
 DT 26-FEB-2002 (first entry)  
 XX  
 DE Human P2Y-like G protein-coupled receptor.  
 XX  
 KW Human; P2Y-like G protein-coupled receptor; GPCR; COPD;  
 KW chronic obstructive pulmonary disease; nervous system disease;  
 KW Parkinson's disease; multiple sclerosis; dementia; stroke;  
 KW Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;  
 KW bacterial infection; fungal infection; protozoan infection;  
 KW viral infection; pain; cancer; anorexia; bulimia; asthma;  
 KW acute heart failure; hypotension; hypertension; osteoporosis; diabetes;  
 KW angina pectoris; myocardial infarction; ulcer; inflammation; allergy;

KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
 KW manic depression; delirium; severe mental retardation; dyskinesia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200185764-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 09-MAY-2001; 2001WO-EP005244.  
 XX  
 PR 11-MAY-2000; 2000US-0203582P.  
 PR 21-FEB-2001; 2001US-0269857P.  
 XX  
 PA (FARB ) BAYER AG.  
 XX  
 PI Ramakrishnan S;  
 XX  
 DR WPI; 2002-075242/10.  
 DR N-PSDB; AAS17746.  
 XX  
 PT New polynucleotides for producing P2Y-like G protein-coupled receptors  
 PT (GPCR) that are used for screening inhibitors or regulators of human P2Y-  
 PT like GPCR, especially useful for treating pain, cancer or neurological  
 PT disorders.  
 PS  
 XX Claim 25; Fig 2; 114pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide encoding a P2Y-like G  
 CC protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or  
 CC allele, a host cell containing an expression vector comprising the  
 CC polynucleotide and screening for agents that regulate the GPCR activity.  
 CC The polynucleotide is useful for producing P2Y-like GPCR polypeptide, human  
 CC which may be employed for screening agents that inhibit or regulate human  
 CC P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is  
 CC useful for treating or ameliorating P2Y-like GPCR disorders, particularly  
 CC COPD (chronic obstructive pulmonary disease), peripheral or central  
 CC nervous system disease (e.g. Parkinson's disease, multiple sclerosis,  
 CC dementia, stroke, Alzheimer's disease and many other diseases and  
 CC disorders listed in the specification), benign prostatic hyperplasia or  
 CC urinary incontinence. A pharmaceutical composition containing the  
 CC modulators and/or regulators of P2Y-like GPCR is useful for modulating  
 CC the activity of a P2Y-like GPCR. In particular, these are useful for  
 CC treating, preventing or ameliorating infections (e.g. bacterial, fungal,  
 CC protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,  
 CC acute heart failure, hypotension, hypertension, osteoporosis, diabetes,  
 CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,  
 CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic  
 CC depression, delirium, severe mental retardation or dyskinesias). The  
 CC present sequence is the P2Y-like GPCR of the invention  
 XX  
 XX Sequence 295 AA;  
 SQ

Query Match 84.8%; Score 1536; DB 5; Length 295;  
 Best Local Similarity 98.3%; Pred. No. 1.9e-160;  
 Matches 283; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVDNMTSQBGLCFQSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60  
 DB 1 MEKVDNMTSQBGLCFQSEKQKVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSGATT 60  
 QY 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLCKLVHFLFYINLYGSILLTLCISVHQ 120  
 DB 61 YLVNLMVADLLVLLPFLIITYSLDDRWPFGECLCKLVHFLFYINLYGSILLTLCISVHQ 120  
 QY 121 FLGVCHPLCSLPYRTRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 180  
 DB 121 FLGVCHPLCSLPYRTRHAWLGSTTTWALVVLQLLPTLAFSHDTYINGQMIWYDMTSOEN 180  
 QY 181 FDRLPAYGIVLTLGSLGFLHGFVLTGQEPDQARGEPHEDROHSPQVHPDPTGVW 240  
 DB 181 FDRLPAYGIVLTLGSLGFLHGFVLTGQEPDQARGEPHEDROHSPQVHPDPTGVW 240

Qy 241 PLHLFCALPVHSLLLPHLLLSAFSLPALDGSQGLQDMASGECEQ 288  
 Db 241 PLHLFCALPVHSLLLPHLLLSAFSLPALDGSQGLQDMASVKAMQ 288

RESULT 5  
 ADI16630  
 ID ADI16630 standard; protein; 361 AA.  
 XX AC ADI16630;  
 XX DT 15-APR-2004 (first entry)  
 XX DE Human NOVX protein to treat human pathological conditions SeqID166.  
 XX KW human; NOVX; cardiomyopathy; atherosclerosis; cancer; diabetes;  
 KW inflammation; autoimmune disorder; allergy; blood disorder;  
 KW acquired immunodeficiency syndrome; AIDS; obesity; asthma;  
 KW immunoglobulin (Ig)A nephropathy; cirrhosis; arthritis;  
 KW Alzheimer's disease; infection; stroke; muscular dystrophy; epilepsy;  
 KW cytosolic; cardiac; antiinflammatory; immunosuppressive; antiallergic;  
 KW haemostatic; anti-HIV; antidiabetic; antiarteriosclerotic; anorectic;  
 KW antiasthmatic; nephrotropic; antiarthritic; hepatotropic;  
 KW neuroprotective; nootropic; antibacterial; virucide; antiparasitic;  
 KW relaxant; anticonvulsant; neurogenesis; wound healing; angiogenesis;  
 KW chromosome mapping; tissue typing; pharmacogenomic; SNP;  
 KW single nucleotide polymorphism.  
 XX OS Homo sapiens.  
 XX PN WO200268649-A2.  
 XX PD 06-SEP-2002.  
 XX PF 31-JAN-2002; 2002WO-US002785.  
 XX PR 31-JAN-2001; 2001US-02853395P.  
 PR 31-JAN-2001; 2001US-0285442P.  
 PR 31-JAN-2001; 2001US-0265514P.  
 PR 31-JAN-2001; 2001US-0265517P.  
 PR 02-FEB-2001; 2001US-0266406P.  
 PR 05-FEB-2001; 2001US-0266767P.  
 PR 07-FEB-2001; 2001US-0266975P.  
 PR 07-FEB-2001; 2001US-0267057P.  
 PR 08-FEB-2001; 2001US-0267459P.  
 PR 09-FEB-2001; 2001US-0267823P.  
 PR 15-FEB-2001; 2001US-0268974P.  
 PR 26-FEB-2001; 2001US-0271664P.  
 PR 27-FEB-2001; 2001US-0271839P.  
 PR 27-FEB-2001; 2001US-0271855P.  
 PR 02-MAR-2001; 2001US-0272788P.  
 PR 02-MAR-2001; 2001US-0273046P.  
 PR 14-MAR-2001; 2001US-0275925P.  
 PR 14-MAR-2001; 2001US-0275947P.  
 PR 14-MAR-2001; 2001US-0275950P.  
 PR 14-MAR-2001; 2001US-0275989P.  
 PR 15-MAR-2001; 2001US-0276448P.  
 PR 15-MAR-2001; 2001US-0276450P.  
 PR 16-MAR-2001; 2001US-0276397P.  
 PR 16-MAR-2001; 2001US-0276768P.  
 PR 20-MAR-2001; 2001US-0276852P.  
 PR 26-MAR-2001; 2001US-0278775P.  
 PR 26-MAR-2001; 2001US-0278778P.  
 PR 29-MAR-2001; 2001US-0279882P.  
 PR 29-MAR-2001; 2001US-0279884P.  
 PR 30-MAR-2001; 2001US-0280147P.  
 PR 11-APR-2001; 2001US-0282992P.  
 PR 11-APR-2001; 2001US-0283083P.  
 PR 20-APR-2001; 2001US-0285133P.  
 PR 23-APR-2001; 2001US-0285749P.  
 PR 03-MAY-2001; 2001US-0288327P.  
 PR 03-MAY-2001; 2001US-0288504P.  
 PR 29-MAY-2001; 2001US-0294047P.

PR 30-MAY-2001; 2001US-0294473P.  
 PR 08-JUN-2001; 2001US-0296964P.  
 PR 18-JUN-2001; 2001US-0298959P.  
 PR 19-JUN-2001; 2001US-0299324P.  
 PR 13-AUG-2001; 2001US-0312020P.  
 PR 16-AUG-2001; 2001US-0312889P.  
 PR 16-AUG-2001; 2001US-0312908P.  
 PR 21-AUG-2001; 2001US-0313390P.  
 PR 28-AUG-2001; 2001US-0315470P.  
 PR 31-AUG-2001; 2001US-0316447P.  
 PR 07-SEP-2001; 2001US-0318115P.  
 PR 07-SEP-2001; 2001US-0318118P.  
 PR 12-SEP-2001; 2001US-0318740P.  
 PR 19-SEP-2001; 2001US-0323379P.  
 PR 18-OCT-2001; 2001US-0330245P.  
 PR 18-OCT-2001; 2001US-0330308P.  
 PR 14-NOV-2001; 2001US-0332701P.  
 XX (CURA-) CURAGEN CORP.  
 PA Tthernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shinkets RA;  
 XX Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CB;  
 PI Gerlach VL, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;  
 PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;  
 XX WPI; 2002-706998/76.  
 DR N-PSDB; ADI16629.  
 XX PT New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.  
 XX PS Claim 1; SEQ ID NO 166; 1498pp; English.  
 XX CC This invention relates to a novel nucleic acids, and encoded polypeptides  
 CC thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOVX proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The NOVX polypeptides, polynucleotides and antibodies are useful in  
 CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,  
 CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in  
 CC treating or preventing diseases such as inflammation, autoimmune  
 CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome  
 CC (AIDS), obesity, asthma, immunoglobulin (Ig)A nephropathy, cirrhosis,  
 CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy,  
 CC and epilepsy. Accordingly, these molecules have many activities including  
 CC cytosolic, cardiac, antiinflammatory, immunosuppressive, antiallergic,  
 CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,  
 CC antiasthmatic, nephrotropic, antiarthritic, hepatotropic,  
 CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,  
 CC relaxant and anticonvulsant. In addition, they are useful in screening  
 CC assays to identify small molecules that modulate or inhibit, for example,  
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
 CC used as in chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. This polypeptide is a human NOVX protein of the  
 CC invention.  
 XX SQ Sequence 361 AA;  
 SQ Query Match 77.1%; Score 1397; DB 5; Length 361;  
 Best Local Similarity 80.9%; Pred. No. 5.5e-145;  
 Matches 275; Conservative 11; Mismatches 40; Indels 14; Gaps 5;  
 Qy 1 MEKVDMNTSQEQGLQCFSEKFKQVYLSLAYSIIFILGLPLNGTVLWHFGQTKWSCATT 60  
 Db 29 MEKVDMNTSQEQGLQCFSEKFKQVYLSLAYSIIFILGLPLNGTVLWHFGQTKWSCATT 88  
 Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGLCKLVHFLFYINLYGSIILLTICISVHQ 120

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      |||
89  YLVNLMWADLLVLLPFLIITVSLDDRWPFGLCKLVHFLFYINLYGSILLTCTISVHQ 148
      |||
121  FLGVCHPLCSLPYRRRHAWLGSTTWALVVLQLLPTLAFSTHDYINGOMIWDMTSOEN 180
      |||
149  FLGVCHPLCSLPYRRRHAWLGSTTWALVVLQLLPTLAFSTHDYINGOMIWDMTSOEN 208
      |||
181  FDLRFAYGIVLTLGSLFLSLGHFGVLTDTGQEPDQARG--EPHEDRQHSQSVHPDHPHG 238
      |||
209  FDLRFAYGIVLTLGSLFLSLGHFGVSL-----WVRSLIKPEENIMRTGNTARARSIRT 262
      |||
239  VMLPFLHF--CALPYHSLLLPHLLSAF---SGLPALDGSQCGLQDMEASGECEQLPQPS 293
      |||
263  ILLVCGLFTLCFVPH-ITRSFYLTICFLSDCQLLMAAQGLQDMEASGECEQLPQPS 321
      |||
294  PVLSPKGGKQNRVLLQKLRQNLGSHHPAGKRCPCGLNRSG 333
      |||
322  PVLSPKGGKQNRVLLQKLRQNLGSHHPAGKRCPCGLNRSG 361

RESULT 6
ADN42284
ID  ADN42284 standard; protein; 361 AA.
XX
AC  ADN42284;
XX
DT  17-JUN-2004 (first entry)
XX
DE  Human novel proteinNOV 43.
XX
KW  Human; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis; SNP;
KW  single nucleotide polymorphism.
XX
OS  Homo sapiens.
XX
FH  Key
FT  Location/Qualifiers
FT  Misc-difference 162
FT  ;/note= "May be Pro as the result of a single nucleotide
FT  polymorphism"
XX
PN  US2004033493-A1.
XX
PD  19-FEB-2004.
XX
PF  31-JAN-2002; 2002US-00072012.
XX
PR  31-JAN-2001; 2001US-0265395P.
PR  31-JAN-2001; 2001US-0265412P.
PR  31-JAN-2001; 2001US-0265514P.
PR  31-JAN-2001; 2001US-0265517P.
PR  02-FEB-2001; 2001US-0266406P.
PR  05-FEB-2001; 2001US-0266767P.
PR  07-FEB-2001; 2001US-0266975P.
PR  07-FEB-2001; 2001US-0267057P.
PR  08-FEB-2001; 2001US-0267459P.
PR  09-FEB-2001; 2001US-0267823P.
PR  15-FEB-2001; 2001US-0268974P.
PR  26-FEB-2001; 2001US-0271664P.
PR  27-FEB-2001; 2001US-0271839P.
PR  27-FEB-2001; 2001US-0271855P.
PR  02-MAR-2001; 2001US-0272788P.
PR  02-MAR-2001; 2001US-0273046P.
PR  14-MAR-2001; 2001US-0275925P.
PR  14-MAR-2001; 2001US-0275947P.
PR  14-MAR-2001; 2001US-0275950P.
PR  14-MAR-2001; 2001US-0275989P.
PR  15-MAR-2001; 2001US-0276448P.
PR  15-MAR-2001; 2001US-0276450P.
PR  16-MAR-2001; 2001US-0276397P.
PR  16-MAR-2001; 2001US-0276768P.
PR  20-MAR-2001; 2001US-0278652P.
PR  26-MAR-2001; 2001US-027875P.
PR  26-MAR-2001; 2001US-0278778P.
      ;

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PR  29-MAR-2001; 2001US-0279882P.
PR  29-MAR-2001; 2001US-0279884P.
PR  30-MAR-2001; 2001US-0280147P.
PR  11-APR-2001; 2001US-0282992P.
PR  11-APR-2001; 2001US-0283083P.
PR  20-APR-2001; 2001US-0285133P.
PR  23-APR-2001; 2001US-0285749P.
PR  03-MAY-2001; 2001US-0288327P.
PR  03-MAY-2001; 2001US-0288504P.
PR  29-MAY-2001; 2001US-0294047P.
PR  30-MAY-2001; 2001US-0294473P.
PR  08-JUN-2001; 2001US-0296964P.
PR  18-JUN-2001; 2001US-0298959P.
PR  19-JUN-2001; 2001US-0299324P.
PR  13-AUG-2001; 2001US-0312020P.
PR  16-AUG-2001; 2001US-0312889P.
PR  16-AUG-2001; 2001US-0312908P.
PR  21-AUG-2001; 2001US-0313930P.
PR  28-AUG-2001; 2001US-0315470P.
PR  31-AUG-2001; 2001US-0316447P.
PR  07-SEP-2001; 2001US-0318115P.
PR  07-SEP-2001; 2001US-0318118P.
PR  12-SEP-2001; 2001US-0318740P.
PR  19-SEP-2001; 2001US-0323379P.
PR  18-OCT-2001; 2001US-0330245P.
PR  18-OCT-2001; 2001US-0330308P.
PR  14-NOV-2001; 2001US-0332701P.
XX
(TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) Li L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTAK K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
XX
Tchernev VT, Spytek KA, Zerhusen BD, Patturajan M, Shimkets RA;
PI Li L, Gangolli EA, Padigar M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CE;
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
WPI; 2004-180039/17.
DR N-PSDB; ADN42283.
DR
XX
PT Isolated NOVX polypeptides and polynucleotides, useful for preventing
PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
PT atherosclerosis.
XX
Claim 1; SEQ ID NO 166; 1309pp; English.
PS
CC The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
CC including splice variants) and the nucleic acids (NA) that encode them.
CC Also included are the mature NOVX proteins (and their encoding
CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
CC vector, an antibody that binds immunospecifically to NOVX, determining
CC the presence or amount of NOVX in a sample, determining the presence or
CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,

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CC modulating the activity of NOVX, treating or preventing a NOVX-associated  
CC disorder, determining the presence of or predisposition to a disease  
CC associated with altered levels of NOVX and treating a pathological state  
CC in a mammal comprising administering a polypeptide which is at least 95%  
CC identical to NOVX (or fragment). NOVX and NA may be used in the  
CC prevention, treatment and diagnosis of diseases associated with  
CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,  
CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and  
CC antagonists may also be used to down regulate expression and activity of  
CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for  
CC detecting the presence of NOVX in samples (e.g. by enzyme linked  
CC immunosorbant assay (ELISA). The agents and methods may be used in this  
CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy  
CC and/or atherosclerosis. The present sequence represents a NOVX protein.  
XX  
XX  
SQ Sequence 361 AA;

Query Match 76.5%; Score 1387; DB 8; Length 361;  
Best Local Similarity 80.6%; Pred. No. 7e-144;  
Matches 274; Conservative 11; Mismatches 41; Indels 14; Gaps 5;  
Qy 1 MEKVDNMTSQBQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60  
Db 29 MEKVDNMTSQBQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88  
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 120  
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 148  
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTWALVQLPLTAFSHDYINGQMIWYDWTQSEN 180  
Db 149 FLGVSHPLCSLPYRTRHAWLGTSTWALVQLPLTAFSHDYINGQMIWYDWTQSEN 208  
Qy 181 FDLRFAYGIVLTSGFLSLGHFGVLEFTDQEPDQARG--EPHEDRQHSPSPHPDPTG 238  
Db 209 FDLRFAYGIVLTSGFLSLGHFGVSL-----WVRSLIKPEENLRMTGNARARSIRT 262  
Qy 239 VWPLHPLF--CALPYHSLLLPHLLSAP---SGLPALDGSQGLQDMEASGECEQLPQPS 293  
Db 263 ILLVCGFLTLCFVFPFH-ITRSFYLTICFLLSQDCQLLMAAQGLQDMEASGECEQLPQPS 321  
Qy 294 PVLSFKGKGNRVLLQKLRQNKLGHPAGRKRCPCPLNRSG 333  
Db 322 PVLSFKGKGNRVLLQKLRQNKLGHPAGRKRCPCPLNRSG 361

RESULT 7  
ADC26009  
ID ADC26009 standard; protein; 338 AA.  
XX  
AC ADC26009;  
XX  
DT 18-DEC-2003 (first entry)  
XX  
DE Human purinergic receptor P2Y-related GPCRx6 alternative protein.  
XX  
KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;  
KW anorectic; cardiant; hypotensive; osteopathic; antianginal;  
KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;  
KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;  
KW GPCR; viral; fungal; bacterial infection; immune-related disorder;  
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;  
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;  
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;  
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;  
KW human; GPCRx6; purinergic receptor P2Y.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 270  
FT /note= "Encoded by TTC"  
XX

PN US2003088080-A1.  
XX  
XX 08-MAY-2003.  
PD  
PF 21-JUN-2001; 2001US-00885453.  
XX  
PR 20-JUN-2000; 2000US-0212908P.  
PR 05-DEC-2000; 2000EP-00870289.  
XX  
XX (COMM// COMMUNI D.  
PA (LANN// LANN V.  
PA (GOVA// GOVAERTS C.  
PA (PARM// PARMENTIER M.  
PA (DETH// DETHUX M.  
XX  
PI Communi D, Lannoy V, Govaerts C, Parmentier M, Dethaux M;  
XX  
XX WPI; 2003-657983/62.  
DR N-PSDB; ADC25999.  
XX  
XX New human G-protein coupled receptor, useful for treating receptor-  
PT mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,  
PT acute heart failure, osteoporosis, stroke, ulcer, allergy, or  
PT neurological disorders.  
XX  
PS Example 3; Page 15; 24pp; English.  
XX  
XX The invention relates to a novel G-protein coupled receptor (GPCR). The  
CC receptor, polynucleotide, agonist, reverse agonist and antagonist of the  
CC invention may be useful for treating receptor-mediated disorders  
CC including viral, fungal or bacterial infections, immune-related disorders  
CC such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,  
CC hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,  
CC ulcer and allergy, as well as psychotic and neurological disorders such  
CC as schizophrenia and dementia, degenerative diseases such as Parkinson's  
CC disease and Alzheimer's disease and dyskinesias such as Huntington's  
CC disease. The current sequence is that of the human purinergic receptor  
CC P2Y-related GPCRx6 alternative protein of the invention.  
XX  
SQ Sequence 338 AA;  
Query Match 58.0%; Score 1051; DB 7; Length 338;  
Best Local Similarity 98.0%; Pred. No. 8.1e-107;  
Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 MEKVDNMTSQBQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60  
Db 29 MEKVDNMTSQBQGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88  
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 120  
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSILLTLCISVHQ 148  
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTWALVQLPLTAFSHDYINGQMIWYDWTQSEN 180  
Db 149 FLGVCHPLCSLPYRTRHAWLGTSTWALVQLPLTAFSHDYINGQMIWYDWTQSEN 208  
Qy 181 FDLRFAYGIVLTSGFLSL 200  
Db 209 FDLRFAYGIVLTSGFLSPPSL 228  
RESULT 8  
ABW00804  
ID ABW00804 standard; protein; 338 AA.  
XX  
AC ABW00804;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Human GPCRx6 protein.  
XX  
KW Human; G-protein coupled receptor; GPCR; infection; neoplastic process;

KW inflammation; myocardial infarction; atherosclerosis; angina pectoris;  
 KW hypertension; osteoporosis; antibacterial; cytostatic; fungicide; pain;  
 KW diabetes; cancer; virucide; analgesic; cardiant.

XX Homo sapiens.

OS US2003108986-A1.

XX US2003108986-A1.

XX 12-JUN-2003.

XX 20-FEB-2002; 2002US-00079384.

XX 21-JUN-2001; 2001US-00885453.

XX (EURO-) EUROSREEN SA.

XX Communi D, Lannoy V, Brezillon S, Detheux M, Parmentier M;

PI Govaerts C;

XX WPI; 2003-810852/76.

DR N-PSDB; AAD61648.

XX Novel G-protein coupled receptor useful for treating viral infections,  
 PT bacterial infections, fungal infections, cancer, diabetes, hypertension,  
 PT osteoporosis, angina pectoris, myocardial infarction, atherosclerosis.

PS Claim 1; Fig 4; Opp; English.

XX The present invention relates to novel G-protein coupled receptors  
 CC (GPCRs) and the nucleic acids encoding them. The invention is useful for  
 CC treating viral, bacterial and fungal infections, inflammatory and  
 CC neoplastic processes, pain, diabetes, hypertension, osteoporosis, cancer,  
 CC angina pectoris, myocardial infarction and atherosclerosis. The present  
 CC sequence is human G-protein coupled receptor (GPCR) protein

XX Sequence 338 AA;

Query Match 58.0%; Score 1051; DB 7; Length 338;  
 Best Local Similarity 98.0%; Pred. No. 8.1e-107;  
 Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MEKVDNMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHPWGQTKRWSCATT 60

Db 29 MEKVDNMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHPWGQTKRWSCATT 88

QY 61 YLVNLMWADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCSVHQ 120

Db 89 YLVNLMWADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCSVHQ 148

QY 121 FLGVCHPLCSLPYRTRRHAWLGSTTWTWLVLLQPLTAFSHTDYINGQMIWYDNTSOEN 180

Db 149 FLGVCHPLCSLPYRTRRHAWLGSTTWTWLVLLQPLTAFSHTDYINGQMIWYDNTSOEN 208

QY 181 FDRLFAYGIVLTSLGFLSLL 200

Db 209 FDRLFAYGIVLTSLGFFPSL 228

RESULT 9

ABB98146

ID ABB98146 standard; protein; 339 AA.

XX ABB98146;

XX 17-OCT-2002 (first entry)

XX Human GPCR designated PFI-020'.

XX Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;

XX gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;

XX disorder; PFI-020'.

XX Homo sapiens.

XX EP1215214-A1.

XX 19-JUN-2002.

XX 04-DEC-2001; 2001EP-00310137.

XX 18-DEC-2000; 2000GB-00030855.

XX 17-JAN-2001; 2001GB-00001222.

XX (PFI-020) PFIZER LTD.

XX (PFI-020) PFIZER INC.

XX Fidoock MD;

XX WPI; 2002-510798/55.

DR N-PSDB; ABQ79300.

XX New polynucleotide encoding G protein-coupled receptor PFI-020, useful  
 PT e.g. for treating eating and sleeping disorders and for identifying  
 PT specific modulators.

XX Claim 1 (b); Page 13; 23pp; English.

XX The invention relates to an isolated polynucleotide encoding a novel  
 CC polypeptide belonging to the class of proteins known as G-protein coupled  
 CC receptors (GPCRs). The activity of proteins of the invention may be  
 CC described as, antidepressant and neuroleptic. Polynucleotides of the  
 CC invention are used for recombinant expression of the G protein-coupled  
 CC receptor (PFI-020) polypeptides, to create transgenic animals, as source  
 CC of primers, probes, antisense sequences and ribozymes and in gene  
 CC therapy. Therapeutic agents of the invention can be used to treat a wide  
 CC range of disorders, particularly mood disorders, depression or arousal,  
 CC especially eating and sleeping disorders. The current sequence represents  
 CC a human GPCR designated PFI-020'

XX Sequence 339 AA;

Query Match 57.8%; Score 1047; DB 5; Length 339;  
 Best Local Similarity 99.0%; Pred. No. 2.3e-106;  
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MEKVDNMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHPWGQTKRWSCATT 60

Db 29 MEKVDNMTSQEGLQCFSEKQKQVYLSLAYSIIFILGLPLNGTVLWHPWGQTKRWSCATT 88

QY 61 YLVNLMWADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCSVHQ 120

Db 89 YLVNLMWADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTCSVHQ 148

QY 121 FLGVCHPLCSLPYRTRRHAWLGSTTWTWLVLLQPLTAFSHTDYINGQMIWYDNTSOEN 180

Db 149 FLGVCHPLCSLPYRTRRHAWLGSTTWTWLVLLQPLTAFSHTDYINGQMIWYDNTSOEN 208

QY 181 FDRLFAYGIVLTSLGFLS 198

Db 209 FDRLFAYGIVLTSLGFLS 226

RESULT 10

AAE18640

ID AAE18640 standard; protein; 339 AA.

XX AAE18640;

XX 17-MAY-2002 (first entry)

XX Human G-protein coupled receptor (GCREC-1).

XX Human; G-protein coupled receptor; GCREC-1; cell proliferative disorder;

XX neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory;

XX metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease;

XX Pick's disease; Huntington's disease; Parkinson's disease; hypertension;



atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic; osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS; anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening; transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant; neutropic; neuroprotective; cardiac; immunosuppressive; anorectic; virucide; receptor.

XX Homo sapiens.

XX Key Location/Qualifiers  
PH Domain 89..109 /note= "Transmembrane domain"  
PT Domain 130..149 /note= "Transmembrane domain"

PT WO200210387-A2.

XX 07-FEB-2002.

XX 25-JUL-2001; 2001WO-US023433.

XX 27-JUL-2000; 2000US-0221478P.

PR 03-AUG-2000; 2000US-0223268P.

PR 21-AUG-2000; 2000US-0227054P.

PR 08-SEP-2000; 2000US-0231121P.

PR 13-SEP-2000; 2000US-0232243P.

PR 15-SEP-2000; 2000US-0232691P.

PR 22-SEP-2000; 2000US-0235146P.

XX (INCY-) INCYTE GENOMICS INC.

XX Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR; PI Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA; PI Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Gaul RC; PI Warren BA, Lee EA, Ding L;

XX WPI; 2002-188744/24.

DR N-PSDB; AAD29667.

XX New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic disorders.

XX Claim 1; Page 114-115; 150pp; English.

XX The invention relates to novel human G-protein coupled receptors (GCREC) and their encoding polynucleotides. GCREC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCREC is useful for diagnosing, treating and preventing a cell proliferative disorder (e.g., hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), gastrointestinal disorder (e.g., gastritis, cirrhosis, Crohn's disease), an autoimmune/ inflammatory disorder (e.g., acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma, rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity, osteoporosis), and viral infections. GCREC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. GCREC is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. GCREC is useful in Southern or Northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, microformat enzyme linked immunosorbant (ELISA)-like assays, and in microarrays utilising fluids or tissues from patients to detect altered GCREC expression. The present sequence is human GCREC-1

XX Sequence 339 AA;

Query Match 57.8%; Score 1047; DB 5; Length 339;  
Best Local Similarity 99.0%; Pred. No. 2.3e-106;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 MEKVDNMTSBOGLQCFSEKVKQVYLSLAYSIIFILGPLNGTVLWHFWGQTKRWSGATT 60  
Db 29 MEKVDNMTSBOGLQCFSEKVKQVYLSLAYSIIFILGPLNGTVLWHFWGQTKRWSGATT 88  
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRPFGEGLCKLVHFLFYINLYGSIILLTFCISVHQ 120  
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRPFGEGLCKLVHFLFYINLYGSIILLTFCISVHQ 148  
Qy 121 FLGVCHPLCSIPYRTRRHAWLGTSTTWALVLOLLPTLAFSHTDYINGQMIWYDMTSQEN 180  
Db 149 FLGVWHPLCSLPYRTRRHAWLGTSTTWALVLOLLPTLAFSHTDYINGQMIWYDMTSQEN 208  
Qy 181 FDLRFAYGIVLTLSGFLS 198  
Db 209 FDLRFAYGIVLTLSGFLS 226

RESULT 11

ADO30394

ID ADO30394 standard; protein; 339 AA.

XX ADO30394;

DT 29-JUL-2004 (first entry)

XX Human GPCR P2Y3L, SEQ ID NO:1497.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytosatic; antiinflammatory; vasotropic; antidiagonal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
KW receptor.

XX Homo sapiens.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;

PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;

XX WPI; 2004-390329/36.

XX N-PSDB; ADO30395.

XX Novel mammalian G protein coupled receptors, useful for identifying compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 1497; 542pp; English.

CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia;  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the  
 CC invention. Note: The full sequence data for this patent did not form part  
 CC of the printed specification; those sequences not shown were obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 339 AA;

Query Match 57.8%; Score 1047; DB 8; Length 339;  
 Best Local Similarity 99.0%; Pred. No. 2.3e-106;  
 Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQOGLQCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60  
 Db 29 MEKVDMTSQOGLQCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88

Qy 61 YLVNLMWADLLVLLPFLIITYSLDDRRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQ 120  
 Db 89 YLVNLMWADLLVLLPFLIITYSLDDRRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQ 148

Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDNTSQEN 180  
 Db 149 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDNTSQEN 208

Qy 181 FDLRFAYGIVLTLSGFLS 198  
 Db 209 FDLRFAYGIVLTLSGFLS 226

RESULT 12

ADC26000  
 ID ADC26000 standard; protein; 338 AA.

AC ADC26000;

DT 18-DEC-2003 (first entry)

DE Human purinergic receptor P2Y-related GPCR $\alpha$ 6 protein.

XX virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;  
 KW anorectic; cardiant; hypotensive; osteopathic; antianginal;  
 KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;  
 KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;  
 KW GPCR; viral; fungal; bacterial infection; immune-related disorder;  
 KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;  
 KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;  
 KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;

KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;  
 KW human; GPCR $\alpha$ ; purinergic receptor P2Y.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Misc-difference 62 /note= "Encoded by TTT"  
 FT Misc-difference 243 /note= "Encoded by AAG"

XX US2003088080-A1.

PD 08-MAY-2003.

XX 21-JUN-2001; 2001US-00885453.

XX 20-JUN-2000; 2000US-0212908P.

XX 05-DEC-2000; 2000EP-00870289.

XX (COMM/) COMMUNI D.

XX (LANV/) LANNOY V.

XX (GOVA/) GOVAERTS C.

XX (PARM/) PARMENTIER M.

XX (DETH/) DETHEUX M.

XX Communi D, Lannoy V, Govaerts C, Parmentier M, Detheux M;

XX WPI; 2003-657983/62.

XX N-PSDB; ADC25999.

XX New human G-protein coupled receptor, useful for treating receptor-mediated disorders, e.g. infections, cancer, pain, diabetes, obesity, acute heart failure, osteoporosis, stroke, ulcer, allergy, or neurological disorders.

XX Example 3; Page 15-16; 24pp; English.

XX The invention relates to a novel G-protein coupled receptor (GPCR). The receptor, polynucleotide, agonist, reverse agonist and antagonist of the invention may be useful for treating receptor-mediated disorders including viral, fungal or bacterial infections, immune-related disorders such as cancer, pain, diabetes, obesity, anorexia, acute heart failure, hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke, ulcer and allergy, as well as psychotic and neurological disorders such as schizophrenia and dementia, degenerative diseases such as Parkinson's disease and Alzheimer's disease and dyskinesias such as Huntington's disease. The current sequence is that of the human purinergic receptor P2Y-related GPCR $\alpha$ 6 protein of the invention.

XX Sequence 338 AA;

Query Match 57.5%; Score 1041; DB 7; Length 338;  
 Best Local Similarity 97.5%; Pred. No. 1e-105;  
 Matches 195; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQOGLQCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60  
 Db 29 MEKVDMTSQOGLQCFSEKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88

Qy 61 YLVNLMWADLLVLLPFLIITYSLDDRRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQ 120  
 Db 89 YLVNLMWADLLVLLPFLIITYSLDDRRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQ 148

Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDNTSQEN 180  
 Db 149 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDNTSQEN 208

Qy 181 FDLRFAYGIVLTLSGFLS 200  
 Db 209 FDLRFAYGIVLTLSGFLS 228

```
RESULT 13
ADC86167
ID  ADC86167 standard; protein; 271 AA.
XX
XX  AC  ADC86167;
XX
XX  DT  01-JAN-2004 (first entry)
XX
XX  DE  Human GPCR protein SEQ ID NO:620.
XX
XX  KW  human; GPCR; guanosine triphosphate-binding protein coupled receptor;
XX  KW  gene therapy.
XX
XX  OS  Homo sapiens.
XX
XX  PN  EP1270724-A2.
XX
XX  PD  02-JAN-2003.
XX
XX  PF  18-JUN-2002; 2002EP-00013517.
XX
XX  PR  18-JUN-2001; 2001JP-00246789.
XX
XX  PA  (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX  PA  (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX
XX  PI  Suwa M, Asai K, Akiyama Y, Aburatani H;
XX
XX  DR  WPI; 2003-315783/31.
XX
XX  DR  N-PSDB; ADC86166.
XX
XX  PS  Claim 2; SEQ ID NO 620; 28pp; English.
XX
XX  CC  The invention relates to a novel polynucleotide encoding a guanosine
XX  CC  triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX  CC  the invention may have a use in gene therapy. The polynucleotide and
XX  CC  polypeptide are useful for preparing a composition for treating a patient
XX  CC  in need of increased or suppressed activity or expression of the
XX  CC  guanosine triphosphate-binding protein coupled receptor. The protein
XX  CC  sequences shown in ADC85549-ADC87617 represent GPCR's of the invention.
XX
XX  SQ  Sequence 271 AA;

Query Match          51.7%; Score 936; DB 7; Length 271;
Best Local Similarity 86.0%; Pred. No. 3e-94;
Matches 178; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Qy  1 MEKVDNMNTSQBGLCFSEKTKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db  1 MEKVDNMNTSQBGLCFSEKTKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Qy  61 YLVNLMVADLLYVLLPELLIITYSDRRPFGELICKLVHFLFYINLYGSIILLTLCISVHQ 120
Db  61 YLVNLMVADLLYVLLPELLIITYSDRRPFGELICKLVHFLFYINLYGSIILLTLCISVHQ 120
Qy  121 FLGVCHPLCSLPYTRRHAWLGSTTWALVQLLPTLAFSHTDYINGQMIWDMTSQEN 180
Db  121 FLGVCHPLCSLPYTRRHAWLGSTTWALVQLLPTLAFSHTDYINGQMIWDMTSQEN 180
Qy  181 FDRLFAYGIVLTLSGFSLSLGHFGVLF 207
Db  181 LMRGTNTARARSIRTIILLVCGLFTLCF 207

RESULT 14
AAG80935
ID  AAG80935 standard; protein; 170 AA.
XX
XX  AC  AAG80935;
```

```
XX
DT  28-AUG-2001 (first entry)
XX
DE  Human nGPCR12.
XX
XX  KW  G protein-coupled receptor; nGPCR; seven transmembrane receptor;
XX  KW  signal transduction; schizophrenia; thyroid disorder; renal failure;
XX  KW  rheumatoid arthritis; CNS disorder; infection; metabolic disease;
XX  KW  cardiovascular disease; proliferative disorder; hormonal disorder;
XX  KW  neurological disorder; neuronal disorder; Alzheimer's disease; cancer;
XX  KW  attention deficit-hyperactivity disorder/attention deficit disorder;
XX  KW  Parkinson's disease; migraine; senile dementia; inflammatory disease;
XX  KW  rheumatoid arthritis; autoimmune disorder; respiratory ailment;
XX  KW  neuroprotective.
XX
XX  OS  Homo sapiens.
XX
XX  PN  WO200136473-A2.
XX
XX  PD  25-MAY-2001.
XX
XX  PF  16-NOV-2000; 2000WO-US031581.
XX
XX  PR  16-NOV-1999; 99US-0165838P.
XX  PR  17-NOV-1999; 99US-0166071P.
XX  PR  19-NOV-1999; 99US-0166678P.
XX  PR  28-DEC-1999; 99US-0173396P.
XX  PR  22-FEB-2000; 2000US-0184129P.
XX  PR  28-FEB-2000; 2000US-0185421P.
XX  PR  28-FEB-2000; 2000US-0185554P.
XX  PR  02-MAR-2000; 2000US-0186530P.
XX  PR  03-MAR-2000; 2000US-0186811P.
XX  PR  09-MAR-2000; 2000US-0188114P.
XX  PR  17-MAR-2000; 2000US-0190310P.
XX  PR  21-MAR-2000; 2000US-0190800P.
XX  PR  20-APR-2000; 2000US-0198568P.
XX  PR  02-MAY-2000; 2000US-0201190P.
XX  PR  08-MAY-2000; 2000US-0203111P.
XX  PR  23-MAY-2000; 2000US-0207094P.
XX
XX  PA  (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX  PI  Vogeli G, Wood LS, Parodi LA, Hiebsch RR, Lind P, Slightom J;
XX  PI  Schellin KA, Kaytes PS, Bannigan CM, Ruff V, Sejlitz T, Huff RM;
XX
XX  DR  WPI; 2001-389826/41.
XX  DR  N-PSDB; AAH50975.
XX
XX  PT  New G protein-coupled receptor (nGPCR-x) and its encoding polynucleotide
XX  PT  useful for diagnosing and treating e.g. schizophrenia.
XX
XX  PS  Claim 37; Page 78; 261pp; English.
XX
XX  CC  The present invention relates to novel G protein-coupled receptors
XX  CC  (nGPCR; where x is 1, 3, 4, 5, 9, 11, 12, 14-18, 20, 21, 22, 24, 27, 28,
XX  CC  31-38, 40, 41, 53-60) and their coding sequences. The present sequence is
XX  CC  one such G protein-coupled receptor. GPCRs are also known as seven
XX  CC  transmembrane receptors and function in signal transduction. The nGPCRx
XX  CC  coding sequences are useful for screening a human to diagnose a disorder
XX  CC  affecting the brain or a genetic predisposition, specifically
XX  CC  schizophrenia. nGPCRx are useful for identifying compounds useful for
XX  CC  treating schizophrenia. Detection of nGPCRx in a sample is useful as a
XX  CC  diagnostic tool for diseases or disorders e.g. thyroid disorders, renal
XX  CC  failure, rheumatoid arthritis, CNS disorders, infections such as HIV-1,
XX  CC  metabolic and cardiovascular diseases, proliferative disorders and
XX  CC  hormonal disorders. Modulators of nGPCRx activity have the utility for
XX  CC  treating neurological disorders, including schizophrenia, ADHD/ADD
XX  CC  (attention deficit-hyperactivity disorder/attention deficit disorder),
XX  CC  and neuronal disorders such as Alzheimer's disease, Parkinson's disease,
XX  CC  migraine and senile dementia. Additional disorders include inflammatory
XX  CC  conditions (e.g. Crohn's disease), rheumatoid arthritis, autoimmune
XX  CC  disorders, cancers, respiratory ailments such as asthma, and inflammatory
XX  CC  diseases e.g. inflammatory bowel disease
```

```
XX SQ Sequence 170 AA;
Query Match 50.8%; Score 921; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSILLLT 114
Db 1 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSILLLT 60

Qy 115 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIYD 174
Db 61 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIYD 120

Qy 175 MTSQENFDRLPAYGIVLTLSGFLSLILGHFGVLFTDQGPDPQARGEPHEDR 224
Db 121 MTSQENFDRLPAYGIVLTLSGFLSLILGHFGVLFTDQGPDPQARGEPHEDR 170

RESULT 15
ABG93753
ID ABG93753 standard; protein; 170 AA.
XX AC ABG93753;
XX DT 26-NOV-2002 (first entry)
XX DE Human G protein-coupled receptor protein, beGPCR-seq12.
XX KW Human; receptor; G protein-coupled receptor; GPCR; nGPCR; beGPCR;
KW nG protein coupled receptor; communication; serpentine structure;
KW seven transmembrane receptor; 7TM; mental disorder; diagnosis;
KW genetic predisposition; brain; immune response; gene therapy;
KW anxiety disorder; depression; bipolar disorder; schizophrenia;
KW Huntington's disease; dyskinesia; manic depression; stroke;
KW Parkinson's disease; Alzheimer's disease; diabetes; inflammation; wound;
KW tranquiliser.
XX OS Homo sapiens.
XX PN WO200264789-A1.
XX PD 22-AUG-2002.
XX PF 14-FEB-2001; 2001WO-US004641.
XX PR 14-FEB-2001; 2001WO-US004641.
XX PA (PHAA ) PHARMACIA & UPJOHN CO.
XX PI Lind P, Parodi LA, Vogeli G, Wood LS;
XX DR WPI; 2002-674879/72.
XX DR N-PSDB; ABS70208.
XX PT New nucleic acids and polypeptides of the nG protein-coupled receptor,
XX useful for treating or diagnosing a mental disorder or a disorder
XX affecting the brain, e.g. anxiety disorders, schizophrenia, stroke or
XX Parkinson's disease.
XX PS Example 1; Page 73; 244pp; English.
XX CC The invention discloses an isolated human polypeptide, and encoding
XX nucleic acid, for a G protein-coupled receptor (GPCR), particularly the
XX nG protein coupled receptor-14 (nGPCR-14). GPCRs are vital in the
XX communication between cells and their environment and are characterised
XX by a serpentine structure that passes through the cell membrane seven
XX times, hence the reason such receptors are sometimes called seven
XX transmembrane receptors (7TM). The polynucleotides and polypeptides are
XX useful for identifying an nGPCR allelic variant that correlates with a
XX mental disorder, for isolating an antibody that binds to an epitope of
XX the polypeptide, for identifying a compound that binds the polypeptide or
```

polynucleotide and/or modulates its biological activity, for screening a human subject to diagnose a disorder, or a genetic predisposition to a disorder, affecting the brain or a genetic disposition to the disorder, for identifying compounds useful for the treatment of a mental disorder, and for identifying a compound useful as a modulator of binding between nGPCR-14 and a binding partner of nGPCR-14. The polypeptide is also useful for inducing an immune response in a mammal. The nucleic acid or polypeptide is particularly useful, using gene therapy, for treating e.g. anxiety disorders, depression, bipolar disorder, schizophrenia, Huntington's disease, dyskinesias, manic depression, stroke, Parkinson's disease or Alzheimer's disease. The nucleic acid and polypeptide may also be used for treating diabetes, inflammation or wounds. The sequences presented in ABG93747-ABG93793, ABG93795 and ABG93796 are the nGPCR (also referred to as beGPCR) proteins

XX SQ Sequence 170 AA;

Query Match 50.8%; Score 921; DB 5; Length 170;  
Best Local Similarity 100.0%; Pred. No. 7.2e-93;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 55 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSILLLT 114
Db 1 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRWPFGEILLCKLVHFLFYINLYGSILLLT 60

Qy 115 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIYD 174
Db 61 CISVHQFLGVCHPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIYD 120

Qy 175 MTSQENFDRLPAYGIVLTLSGFLSLILGHFGVLFTDQGPDPQARGEPHEDR 224
Db 121 MTSQENFDRLPAYGIVLTLSGFLSLILGHFGVLFTDQGPDPQARGEPHEDR 170
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Job time : 188 secs

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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:53:44 ; Search time 166 Seconds  
(without alignment)  
838.176 Million cell updates/sec

Title: US-10-088-726-20

Perfect score: 1812

Sequence: 1 MEKVDMTSQGLQCFSEK.....NKLGEHPAGRKRCPLNRSG 333

Scoring table: BLOSUM62

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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA Main:

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- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
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- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
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- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1812	100.0	333	4	US-10-088-726-20
2	1798	99.2	360	4	US-10-023-586B-2
3	1798	99.2	360	4	US-10-763-972-2
4	1536	84.8	295	4	US-10-275-910-2
5	1397	77.1	361	4	US-10-072-012-166
6	1051	58.0	338	3	US-09-885-453-4
7	1047	57.8	339	4	US-10-079-384-6
8	1047	57.8	339	4	US-10-023-586B-4
9	1047	57.8	339	4	US-10-333-946-1
10	1047	57.8	339	4	US-10-763-972-4
11	936	51.7	271	4	US-10-017-161-708
12	936	51.7	271	4	US-10-292-798-620
13	921	50.8	170	3	US-09-782-974C-14
14	921	50.8	170	5	US-10-467-492A-14
15	921	50.8	170	5	US-10-975-979-14
16	921	50.8	170	5	US-10-969-727-14
17	449	24.8	328	4	US-10-010-568-10
18	449	24.8	328	4	US-10-010-568-14
19	449	24.9	328	4	US-10-275-910-3
20	449	24.8	328	4	US-10-375-157-10
21	449	24.8	328	4	US-10-375-157-14
22	449	24.8	328	4	US-10-072-012-519
23	449	24.8	328	4	US-10-072-012-520
24	429	23.7	374	3	US-09-745-842-15
25	429	23.7	374	4	US-10-010-568-11
26	429	23.7	374	4	US-10-375-157-11
27	429	23.7	374	4	US-10-072-012-518

28	424	23.4	537	4	US-10-311-956-4	Sequence 4, Appli
29	424	23.4	537	4	US-10-010-568-12	Sequence 12, Appl
30	424	23.4	537	4	US-10-375-157-12	Sequence 12, Appl
31	424	23.4	537	4	US-10-055-569A-52	Sequence 52, Appl
32	424	23.4	537	4	US-10-072-012-517	Sequence 517, App
33	397	21.9	328	4	US-10-278-087A-39	Sequence 39, Appl
34	396	21.9	361	3	US-09-964-821B-15	Sequence 15, Appl
35	396	21.9	361	4	US-10-010-568-9	Sequence 9, Appli
36	396	21.9	361	4	US-10-268-332-15	Sequence 15, Appli
37	396	21.9	361	4	US-10-375-157-9	Sequence 9, Appli
38	396	21.9	361	4	US-10-072-012-521	Sequence 521, App
39	396	21.9	361	4	US-10-775-965-15	Sequence 15, Appl
40	395.5	21.8	377	3	US-09-745-842-17	Sequence 17, Appl
41	395.5	21.8	377	4	US-10-225-567A-217	Sequence 217, App
42	395.5	21.8	377	5	US-10-756-149-5688	Sequence 5688, Ap
43	394.5	21.8	328	4	US-10-278-087A-56	Sequence 56, Appl
44	389.5	21.5	328	3	US-09-745-842-18	Sequence 18, Appl
45	389.5	21.5	328	4	US-10-225-567A-223	Sequence 223, App

ALIGNMENTS

RESULT 1

US-10-088-726-20  
; Sequence 20, Application US/10088726  
; Publication No. US20030157558A1

; GENERAL INFORMATION:

; APPLICANT: Matsumoto et al.

; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS AI

; FILE REFERENCE: 62514

; CURRENT APPLICATION NUMBER: US/10/088,726

; CURRENT FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: PCT/JP00/09408

; PRIOR FILING DATE: 2000-12-28

; PRIOR APPLICATION NUMBER: JP 1999-375152

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: JP 2000-101339

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 20

; LENGTH: 333

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-10-088-726-20

Query Match 100.0%; Score 1812; DB 4; Length 333;  
Best Local Similarity 100.0%; Pred. No. 1.7e-162;  
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEKVDMTSQGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT	60
Db	1	MEKVDMTSQGLQCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT	60
Qy	61	YLNLWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ	120
Db	61	YLNLWADLLYVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ	120
Qy	121	FLGVCHPLCSLPYTRRHAWLGTSTTWALVVLQLLPTLAFSHDTDYINGQMIWDMTSQEN	180
Db	121	FLGVCHPLCSLPYTRRHAWLGTSTTWALVVLQLLPTLAFSHDTDYINGQMIWDMTSQEN	180
Qy	181	FDRLPAYGIVTLTSGFLSLLGHFGVLFDTGQEPQARGEPHEDRQHSQVHPDHTGW	240
Db	181	FDRLPAYGIVTLTSGFLSLLGHFGVLFDTGQEPQARGEPHEDRQHSQVHPDHTGW	240
Qy	241	PLHPLFCALPYHSLLLPHLLLSA SGLPDLGSCGLQDMEASGECEOLPOPSVLSFGK	300
Db	241	PLHPLFCALPYHSLLLPHLLLSA SGLPDLGSCGLQDMEASGECEOLPOPSVLSFGK	300
Qy	301	GKRVRLQLKRNQKLGEHPAGRKRCPLNRSG	333

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Db 301 GKNRVLQKLRQKLGHPAGRKRCFGLNRS 333
|||||
PRIORITY FILING DATE: 2000-12-18
PRIORITY APPLICATION NUMBER: US 60/260,563
PRIORITY FILING DATE: 2001-01-09
PRIORITY APPLICATION NUMBER: US 60/265,688
PRIORITY FILING DATE: 2001-02-01
PRIORITY APPLICATION NUMBER: GB 0101222.8
PRIORITY FILING DATE: 2001-01-17
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in version 3.2
SEQ ID NO 2
LENGTH: 360
TYPE: PRT
ORGANISM: Homo sapiens
US-10-763-972-2

Query Match 99.2%; Score 1798; DB 4; Length 360;
Best Local Similarity 99.7%; Pred. No. 4.1e-161;
Matches 331; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEKVDNMTSQEGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db 29 MEKVDNMTSQEGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88
Qy 61 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTICISVHQ 120
Db 89 YLVNLMVADLLYVLLPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSIILLTICISVHQ 148
Qy 121 FLGVCHPLCSLPYRTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 180
Db 149 FLGVCHPLCSLPYRTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQEN 208
Qy 181 FDLRFAYGIVLTLSGFLSLILGHFGVLTGQEPDQARGEPEHEDROHSPSOVHPDHPGTGVW 240
Db 209 FDLRFAYGIVLTLSGFLSLILGHFGVLTGQEPDQARGEPEHEDROHSPSOVHPDHPGTGVW 268
Qy 241 PLHPLFCALPYHSLLLPHLLSAPSGLPALDGSQGLQDMASGECEQLPQSPVLSFKG 300
Db 269 PLHPLFCALPYHSLLLPHLLSAPSGLPALDGSQGLQDMASGECEQLPQSPVLSFKG 328
Qy 301 GKNRVLQKLRQKLGHPAGRKRCFGLNRS 332
Db 329 GKNRVLQKLRQKLGHPAGRKRCFGLNRS 360

RESULT 4
US-10-275-910-2
Sequence 2, Application US/10275910
Publication No. US20030166142A1
GENERAL INFORMATION:
APPLICANT: Ramakrishnan, Shyam
TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: 4974.00885
CURRENT APPLICATION NUMBER: US/10/275,910
PRIORITY FILING DATE: 2002-11-12
PRIORITY APPLICATION NUMBER: US 60/203,582
PRIORITY FILING DATE: 2000-05-11
PRIORITY APPLICATION NUMBER: US 60/269,857
PRIORITY FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
LENGTH: 295
TYPE: PRT
ORGANISM: Homo sapiens
US-10-275-910-2

Query Match 84.8%; Score 1536; DB 4; Length 295;
Best Local Similarity 98.3%; Pred. No. 1.8e-136;
Matches 283; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MEKVDNMTSQEGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
Db 1 MEKVDNMTSQEGLCFSEKQKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
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Qy	61	YLVNLMVADLLVLLPFLII	YSLDSDRRWPFGE	LCKLVHFLFYINLYG	SILLTCTISVHQ	120
Db	61	YLVNLMVADLLVLLPFLII	YSLDSDRRWPFGE	LCKLVHFLFYINLYG	SILLTCTISVHQ	120
Qy	121	FLGVCHPLCSLPYRTRRA	WLGTSITTWALVLI	PTLAFSHTD	YINGQMIWDMTSQEN	180
Db	121	FLGVCHPLCSLPYRTRRA	WLGTSITTWALVLI	PTLAFSHTD	YINGQMIWDMTSQEN	180
Qy	181	FDRLFAYGIVLTLSGFL	SLLGHFGVLT	FDGQEPDQARGE	PHEDRQHSPSQVHD	240
Db	181	FDRLFAYGIVLTLSGFL	SLLGHFGVLT	FDGQEPDQARGE	PHEDRQHSPSQVHD	240
Qy	241	PLHPLFCALPYHSLLLP	HHLSAFSGLPALD	GSQCGLQDMEASG	CECSQ	288
Db	241	PLHPLFCALPYHSLLLP	HHLSAFSGLPALD	GSQCGLQDMEASG	CECSQ	288

## RESULT 5

US-10-072-012-166  
; Sequence 166, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zethusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Anderson, David W.  
; APPLICANT: Rastelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr, Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.  
; APPLICANT: Wolenc, Adam R.  
; APPLICANT: Pena, Carol E. A  
; APPLICANT: Furtak, Katarzyna  
; APPLICANT: Grosse, William M.  
; APPLICANT: Alsbobrook II, John P.  
; APPLICANT: Lepley, Denise M.  
; APPLICANT: Rieger, Daniel K.  
; APPLICANT: Burgess, Catherine E.  
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same  
; FILE REFERENCE: 21402-258  
; CURRENT APPLICATION NUMBER: US/10/072,012  
; CURRENT FILING DATE: 2002-01-31  
; PRIOR APPLICATION NUMBER: 60/265,102  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/265,514  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,517  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,412  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/265,395  
; PRIOR FILING DATE: 2001-01-31  
; PRIOR APPLICATION NUMBER: 60/266,406  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 60/266,767  
; PRIOR FILING DATE: 2001-02-05  
; PRIOR APPLICATION NUMBER: 60/267,057  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/266,975  
; PRIOR FILING DATE: 2001-02-07  
; PRIOR APPLICATION NUMBER: 60/267,459  
; PRIOR FILING DATE: 2001-02-08  
; Remaining Prior Application data removed - See File Wrapper  
; NUMBER OF SEQ ID NOS: 1391  
; SOFTWARE: PatentIn Ver. 2.1

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Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208
Qy      181 FDLRFAYGIVLTLSGFLSLL 200
      |||||
Db      209 FDLRFAYGIVLTLSGFFPSL 228

RESULT 7
US-10-079-384-6
; Sequence 6, Application US/10079384
; Publication No. US20030108986A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 9409/2132
; CURRENT APPLICATION NUMBER: US/10/079,384
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-20
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-079-384-6

Query Match      58.0%; Score 1051; DB 4; Length 338;
Best Local Similarity 98.0%; Pred. No. 1.4e-90;
Matches 196; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 MEKVDNMTSQEGLCFSEKYKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
      |||||
Db      29 MEKVDNMTSQEGLCFSEKYKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88

Qy      61 YLVNLMVADLLVLLPLIITYSLDDRWPGEGLCKLVHFLFYINLYGSIILLTLCISVHQ 120
      |||||
Db      89 YLVNLMVADLLVLLPLIITYSLDDRWPGEGLCKLVHFLFYINLYGSIILLTLCISVHQ 148

Qy      121 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 180
      |||||
Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208

Qy      181 FDLRFAYGIVLTLSGFLSLL 200
      |||||
Db      209 FDLRFAYGIVLTLSGFFPSL 228

RESULT 8
US-10-023-586B-4
; Sequence 4, Application US/10023586B
; Publication No. US20030166882A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Ltd. (EP (GB) only)
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)
; APPLICANT: Fidock, Mark David
; TITLE OF INVENTION: No. US20030166882A1el Polypeptide
; FILE REFERENCE: PC10960AGR
; CURRENT APPLICATION NUMBER: US/10/023,586B
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: GB 0030855.1
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/260,563
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: US 60/265,688
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: GB 0101222.8
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 339
; TYPE: PRT

Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208
Qy      181 FDLRFAYGIVLTLSGFLSLL 200
      |||||
Db      209 FDLRFAYGIVLTLSGFFPSL 228

RESULT 9
US-10-333-946-1
; Sequence 1, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAU, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CD1
US-10-333-946-1

Query Match      57.8%; Score 1047; DB 4; Length 339;
Best Local Similarity 99.0%; Pred. No. 3.4e-90;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; ORGANISM: Homo sapiens
US-10-023-586B-4

Query Match      57.8%; Score 1047; DB 4; Length 339;
Best Local Similarity 99.0%; Pred. No. 3.4e-90;
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MEKVDNMTSQEGLCFSEKYKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 60
      |||||
Db      29 MEKVDNMTSQEGLCFSEKYKQVLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATT 88

Qy      61 YLVNLMVADLLVLLPLIITYSLDDRWPGEGLCKLVHFLFYINLYGSIILLTLCISVHQ 120
      |||||
Db      89 YLVNLMVADLLVLLPLIITYSLDDRWPGEGLCKLVHFLFYINLYGSIILLTLCISVHQ 148

Qy      121 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 180
      |||||
Db      149 FLGVCHPLCSLPYRTRRHAWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSQEN 208

Qy      181 FDLRFAYGIVLTLSGFLS 198
      |||||
Db      209 FDLRFAYGIVLTLSGFLS 226

RESULT 9
US-10-333-946-1
; Sequence 1, Application US/10333946
; Publication No. US20040023252A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.
; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.
; APPLICANT: BURFORD, Neil; YUE, Henry
; APPLICANT: GANDHI, Ameena R.; ELLIOTT, Vicki S.
; APPLICANT: RAMKUMAR, Jayalaxmi; BAUGHN, Mariah R.
; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.
; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.
; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.
; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam
; APPLICANT: GRAU, Richard C.; WARREN, Bridget A.
; APPLICANT: LEE, Ernestine A.; DING, Li
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0176 USN
; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CD1
US-10-333-946-1

Query Match      57.8%; Score 1047; DB 4; Length 339;
Best Local Similarity 99.0%; Pred. No. 3.4e-90;
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Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 60  
Db 29 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 88  
Qy 61 YLVNLMVADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120  
Db 89 YLVNLMVADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 148  
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSGEN 180  
Db 149 FLGVWHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSGEN 208  
Qy 181 FDRLFAYGIVLTLGFLS 198  
Db 209 FDRLFAYGIVLTLGFLS 226

## RESULT 10

US-10-763-972-4  
; Sequence 4, Application US/10763972  
; Publication No. US20040137500A1  
; GENERAL INFORMATION:  
; APPLICANT: PFIZER INC.  
; TITLE OF INVENTION: Novel Polypeptide  
; FILE REFERENCE: P10960B  
; CURRENT APPLICATION NUMBER: US/10763.972  
; PRIOR FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: GB 0030855.1  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/260,563  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: US 60/265,688  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: GB 0101222.8  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-763-972-4

Query Match 57.8%; Score 1047; DB 4; Length 339;  
Best Local Similarity 99.0%; Pred. No. 3.4e-90;  
Matches 196; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 60  
Db 29 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 88  
Qy 61 YLVNLMVADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120  
Db 89 YLVNLMVADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 148  
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSGEN 180  
Db 149 FLGVWHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSGEN 208  
Qy 181 FDRLFAYGIVLTLGFLS 198  
Db 209 FDRLFAYGIVLTLGFLS 226

## RESULT 11

US-10-017-161-708  
; Sequence 708, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO

; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; PRIOR FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 708  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-708

Query Match 51.7%; Score 936; DB 4; Length 271;  
Best Local Similarity 86.0%; Pred. No. 7.9e-80;  
Matches 178; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 60  
Db 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 60  
Qy 61 YLVNLMVADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120  
Db 61 YLVNLMVADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120  
Qy 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSGEN 180  
Db 121 FLGVCHPLCSLPYRTRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDWTSGEN 180  
Qy 181 FDRLFAYGIVLTLGFLSGLHGFGLF 207  
Db 181 LMRGTARARSIRINTILLVCGFLTLCF 207

## RESULT 12

US-10-292-798-620  
; Sequence 620, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 620  
; LENGTH: 271  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-620

Query Match 51.7%; Score 936; DB 4; Length 271;  
Best Local Similarity 86.0%; Pred. No. 7.9e-80;  
Matches 178; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 60  
Db 1 MEKVDMTSQEGLCFSEKQVYLSLAYSIIFILGLPLNGTVLWHFWGOTKWSGATT 60  
Qy 61 YLVNLMVADLLVLLPFLIITYSLDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQ 120

Db 61 YLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSIILLTTCISVHQ 120  
Qy 121 FLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYDMSOEN 180  
Db 121 FLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWLIKPEEN 180  
Cy 181 FDLRFAYGIVLTLGSLFLSLGHFGVLF 207  
Db 181 LMRGTGARARSIRTIILLVCGSLFTLCP 207

## RESULT 13

US-09-782-974C-14  
; Sequence 14, Application US/09782974C  
; Publication No. US20030082534A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacacia & Upjohn Company  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis A.  
; TITLE OF INVENTION: Novel G Protein Coupled Receptor  
; FILE REFERENCE: 041USPHRM311  
; CURRENT APPLICATION NUMBER: US/09/782,974C  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 60/165,838  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 09/714,449  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 60/198,568  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,071  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,678  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: 60/173,396  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/184,129  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/185,421  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/185,554  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/186,530  
; PRIOR FILING DATE: 2000-03-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-782-974C-14

Query Match 50.8%; Score 921; DB 3; Length 170;  
Best Local Similarity 100.0%; Pred. No. 1.le-78;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 55 WSCATTYLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSIILLT 114  
Db 1 WSCATTYLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSIILLT 60  
Qy 115 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 174  
Db 61 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 120  
Qy 175 MTSQENFDRLPAYGIVLTLGSLFLSLGHFGVLFDTGQEPDQARGEPEHEDR 224  
Db 121 MTSQENFDRLPAYGIVLTLGSLFLSLGHFGVLFDTGQEPDQARGEPEHEDR 170

## RESULT 14

US-10-467-492A-14  
; Sequence 14, Application US/10467492A

; Publication No. US20050069976A1  
; GENERAL INFORMATION:  
; APPLICANT: Pharmacacia & Upjohn Company  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Lind, Peter  
; APPLICANT: Wood, Linda S.  
; APPLICANT: Parodi, Luis A.  
; TITLE OF INVENTION: Novel G Protein Coupled Receptor  
; FILE REFERENCE: 0411PPHRM313  
; CURRENT APPLICATION NUMBER: US/10/467,492A  
; CURRENT FILING DATE: 2003-08-07  
; NUMBER OF SEQ ID NOS: 192  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-467-492A-14  
Query Match 50.8%; Score 921; DB 5; Length 170;  
Best Local Similarity 100.0%; Pred. No. 1.le-78;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 WSCATTYLVNLMVADLLVLLPFLIIITYSLDDRPFGEELCKLVHFLFYINLYGSIILLT 60  
Qy 115 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 174  
Db 61 CISVHQFLGVCHPLCSLPYRTRRHWLGSTTVALVVLQLLPTLAFSHTDYINGQMIWYD 120  
Qy 175 MTSQENFDRLPAYGIVLTLGSLFLSLGHFGVLFDTGQEPDQARGEPEHEDR 224  
Db 121 MTSQENFDRLPAYGIVLTLGSLFLSLGHFGVLFDTGQEPDQARGEPEHEDR 170  
RESULT 15  
US-10-975-979-14  
; Sequence 14, Application US/10975979  
; Publication No. US20050112660A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Huff, Rita  
; APPLICANT: Sejlitz, Torsten  
; APPLICANT: Lind, Peter  
; APPLICANT: Slightom, Jerry  
; APPLICANT: Schellin, Kathleen  
; APPLICANT: Bannigan, Chris  
; APPLICANT: Ruff, Valerie  
; APPLICANT: Kaytes, Paul  
; APPLICANT: Wood, Linda  
; APPLICANT: Parodi, Luis  
; APPLICANT: Hiebsch, Ronald  
; TITLE OF INVENTION: Novel G Protein Coupled Receptors  
; FILE REFERENCE: 00431PHRM293  
; CURRENT APPLICATION NUMBER: US/10/975,979  
; CURRENT FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: US/09/714,449  
; PRIOR FILING DATE: 2000-11-16  
; PRIOR APPLICATION NUMBER: 60/165,838  
; PRIOR FILING DATE: 1999-11-16  
; PRIOR APPLICATION NUMBER: 60/198,568  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: 60/166,071  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/166,678  
; PRIOR FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: 60/173,396  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/184,129  
; PRIOR FILING DATE: 2000-02-22  
; PRIOR APPLICATION NUMBER: 60/185,421  
; PRIOR FILING DATE: 2000-02-28

; PRIOR APPLICATION NUMBER: 60/185,554  
; PRIOR FILING DATE: 2000-02-28  
; PRIOR APPLICATION NUMBER: 60/186,530  
; PRIOR FILING DATE: 2000-03-02  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 190  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 14  
; LENGTH: 170  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-975-979-14

Query Match 50.8%; Score 921; DB 5; Length 170;  
Best Local Similarity 100.0%; Pred. No. 1.1e-78;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 55 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFPGELCKLVHFLFYINLYGSILLT 114  
Db 1 WSCATTYLVNLMVADLLVLLPFLIITYSLDDRPFPGELCKLVHFLFYINLYGSILLT 60  
  
Qy 115 CISVHQFLGVCPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIWD 174  
Db 61 CISVHQFLGVCPLCSLPYRTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGOMIWD 120  
  
Qy 175 MTSQENFDRLPAYGIVLTLGFLSLGHFGLFTDGPDPQARGEPEHEDR 224  
Db 121 MTSQENFDRLPAYGIVLTLGFLSLGHFGLFTDGPDPQARGEPEHEDR 170

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Job time : 167 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 13, 2006, 14:54:19 ; Search time 16 Seconds  
(without alignments)  
273.113 Million cell updates/sec

Title: US-10-088-726-20

Perfect score: 1812

Sequence: 1 MEKVDMTNSQSGLCQFSEK.....NKLGEHPAGKRCPLNRSRG 333

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08 NEW PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06 NEW PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07 NEW PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT NEW PUB pep.\*  
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7: /cgn2\_6/ptodata/2/pubpaa/US11 NEW PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60 NEW PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	375	20.7	365	6	US-10-995-561-545
2	336	18.5	373	7	US-11-127-877-46
3	257	14.2	339	7	US-11-157-930-4
4	257	14.2	367	7	US-11-157-930-6
5	247	13.6	388	6	US-10-995-561-713
6	247	13.6	394	6	US-10-995-561-714
7	247	13.6	394	6	US-10-995-561-715
8	244	13.5	359	6	US-10-995-561-712
9	244	13.5	359	6	US-10-995-561-716
10	244	13.5	359	7	US-11-127-877-65
11	243.5	13.4	359	6	US-10-876-787-2
12	238	13.1	97	6	US-10-980-388-92
13	234.5	12.9	485	6	US-10-821-234-934
14	227.5	12.6	254	6	US-10-055-877-248
15	227.5	12.6	254	6	US-10-055-877-327
16	227.5	12.6	254	6	US-10-055-877-340
17	227.5	12.6	254	6	US-10-877-346-83
18	226.5	12.5	346	6	US-11-157-930-2
19	224	12.4	349	7	US-11-028-922A-2
20	224	12.4	371	7	US-11-134-811-4
21	224	12.4	371	7	US-11-218-281-2
22	224	12.4	371	7	US-11-218-281-33
23	221.5	12.2	269	7	US-11-151-482-5
24	221.5	12.2	333	7	US-11-127-877-57
25	220.5	12.2	355	7	US-11-218-281-26

26 220 12.1 400 7 US-11-127-877-55 Sequence 55, Appl  
27 218 12.0 371 7 US-11-134-811-6 Sequence 6, Appl  
28 218 12.0 371 7 US-11-218-281-3 Sequence 3, Appl  
29 217.5 12.0 351 7 US-11-218-281-12 Sequence 12, Appl  
30 217.5 12.0 351 7 US-11-218-281-24 Sequence 24, Appl  
31 216 11.9 375 7 US-11-127-877-67 Sequence 67, Appl  
32 214 11.8 360 6 US-10-959-310-36 Sequence 36, Appl  
33 210.5 11.6 371 7 US-11-134-811-2 Sequence 2, Appl  
34 210.5 11.6 373 7 US-11-218-281-1 Sequence 1, Appl  
35 210.5 11.6 373 7 US-11-218-281-28 Sequence 28, Appl  
36 206.5 11.4 352 7 US-11-028-922A-1 Sequence 1, Appl  
37 206 11.4 337 7 US-11-218-281-25 Sequence 25, Appl  
38 205 11.3 337 7 US-11-166-412-60 Sequence 60, Appl  
39 203.5 11.2 259 6 US-10-055-877-225 Sequence 225, App  
40 203.5 11.2 259 6 US-10-055-877-237 Sequence 237, App  
41 203.5 11.2 482 7 US-11-169-976-2 Sequence 2, Appl  
42 203.5 11.2 482 7 US-11-218-281-30 Sequence 30, Appl  
43 202.5 11.2 415 7 US-11-017-058-2 Sequence 2, Appl  
44 201.5 11.1 353 7 US-11-017-058-9 Sequence 9, Appl  
45 200.5 11.1 350 6 US-10-502-145-1 Sequence 1, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-995-561-545  
; Sequence 545, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995.561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 545  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-545

Query Match 20.7%; Score 375; DB 6; Length 365;

Best Local Similarity 41.7%; Pred. No. 1.3e-26;

Matches 80; Conservative 30; Mismatches 74; Indels 8; Gaps 3;

Qy 15 CQSEKQVYLSAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLVYL 74  
Db 27 CWFDEDFKILLPVSYAVVFLGGLNAPTULWLFIRLPWDATATYMFHLALSDTLVL 86  
Qy 75 -LPFLITYSLDDRWPFGEELCKLVHFLFYINLYCSILLTLCISVHQPLGVCHPLCSLPY 133  
Db 87 SLPTLIYYAAHNPFGTEICKFVFLFYWNLYCSVLFLTCISVHYRILGICHPLRALRW 146  
Qy 134 RTRHAMIGTSTTVALVVLQLLPTLASHTDYINGQMIWYDMTSONFDRFLPAYGIVLTL 193  
Db 147 GRPRLAGLLCLAVLWVAGCLVPNLFVFTTSNKGTTVLCHDTRPEEDFHYHFS----- 201  
Qy 194 SGFLSLICHGQV 205  
Db 202 SAVNGLL--FGV 211

##### RESULT 2

US-11-127-877-46  
; Sequence 46, Application US/11127877  
; Publication No. US20050287565A1  
; GENERAL INFORMATION:  
; APPLICANT: Merckhiers, Pascal G.  
; APPLICANT: Hoffmann, Marcel



APPLICANT: Spittäels, Koenraad F. F.  
APPLICANT: Laenen, Wendy  
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting  
FILE OF INVENTION: Amyloid-Beta Protein Production  
FILE REFERENCE: P27,800-B USA  
CURRENT APPLICATION NUMBER: US/11/127,877  
CURRENT FILING DATE: 2005-05-12  
PRIOR APPLICATION NUMBER: 60/570,352  
PRIOR FILING DATE: 2004-05-12  
PRIOR APPLICATION NUMBER: 60/603,948  
PRIOR FILING DATE: 2004-08-24  
NUMBER OF SEQ ID NOS: 590  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 46  
LENGTH: 373  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-127-877-46

Query Match 18.5%; Score 336; DB 7; Length 373;  
Best Local Similarity 30.2%; Pred. No. 4.4e-23;  
Matches 94; Conservative 51; Mismatches 122; Indels 44; Gaps 10;  
Qy 25 YLSLAYSIFRILGLPLNGTVLWHFWGQTKRWSGATTVLVNLMVADLLVYL-LPFLIITYS 83  
Db 53 YLPVAVILVFIIFGLGNSVAIWMFVFMKPMGSGISVTNENALADFLVLTLPALIFYF 112  
Qy 84 LDDRPFGELCKLVHFLFYINLYGSIILLTLCISVHQLGVCHPLCSLPYRTRHAWLGT 143  
Db 113 NKTDWIFGDACKLQRFIFVHNLVYSLIFLTCISAHRYSGVVYPLKSLGLRKKNAICIS 172  
Qy 144 STWALVVLQPLTAFSHDTYINGQMI-WYDWTSONFDRFLFAYGIVLILSGF----LS 198  
Db 173 VLVWLIIVVAISPILFYSGTGVRNKNKTCYDITTSDEYLSRYFTYSMTTAMFCVPLVL 232  
Qy 199 LLGHFGVLFTDGPQDQARGEPHEDROHSPSOVHPDPTGWPPLHPLFCALPYHSL-LLP 257  
Db 233 ILGCYGLI-----VRALIYLDLONSPLRRK-----SYLVIIIVTVFAVSIIYIP 275  
Qy 258 HHLISAFSGPLALD---GSCGLQD-----MEASGECPQLPQSPVLSFKGGKN 303  
Db 276 PHVMTWNLRLARLDQFQTPAMCAFNDRVVATYQVTRGLASLNSC-----VDPILYFLAGDT 330  
Qy 304 -RVLLQKLRQ 313  
Db 331 FRRLSRATRK 341

RESULT 3  
US-11-157-930-4  
Sequence 4, Application US/11157930  
Publication No. US20050266482A1  
GENERAL INFORMATION:  
APPLICANT: Xiao, Yonghong  
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR  
FILE OF INVENTION: Protein  
FILE REFERENCE: 04974.00458  
CURRENT FILING DATE: 2005-06-22  
PRIOR APPLICATION NUMBER: US/11/157,930  
PRIOR FILING DATE: 2005-06-22  
PRIOR APPLICATION NUMBER: US/09/828,478  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 60/195,196  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/254,876  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 339  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-157-930-4

Query Match 14.2%; Score 257; DB 7; Length 339;  
Best Local Similarity 33.0%; Pred. No. 5.2e-16;  
Matches 59; Conservative 34; Mismatches 78; Indels 8; Gaps 2;  
Qy 30 YSIIFILGLPLNGTVLWHFWGQTKRWSGATTVLVNLMVADLLVYL-LPFLIITYSLDDRW 88  
Db 38 YLLDFILALVGNLTALWLFIRDHKSCTPANVFLMHLAVADLSCVVLPTPLVYVHFSGNHW 97  
Qy 89 PFGELCKLVHFLFYINLYGSIILLTLCISVHQLGVCHPLCSLPYRTRHAWLGTSTTWA 148  
Db 98 PFGELCKLVHFLFYINLYGSIILLTLCISADRLFAIVHPVKSLKRLRPLVLAHLACAFW 157  
Qy 149 LVVLQPLTAFSHDTYINGQMIWYDWTSE-----NFDRLFAYGIVLTLGSLFLSLL 200  
Db 158 VVAVAMAPLLVSPQTQVNTHTVVLQLYREKASHALVSLAVAFPTFFITVTCYLLII 216

RESULT 4  
US-11-157-930-6  
Sequence 6, Application US/11157930  
Publication No. US20050266482A1  
GENERAL INFORMATION:  
APPLICANT: Xiao, Yonghong  
TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR  
FILE OF INVENTION: Protein  
FILE REFERENCE: 04974.00458  
CURRENT FILING DATE: 2005-06-22  
PRIOR APPLICATION NUMBER: US/11/157,930  
PRIOR FILING DATE: 2005-06-22  
PRIOR APPLICATION NUMBER: US/09/828,478  
PRIOR FILING DATE: 2001-04-09  
PRIOR APPLICATION NUMBER: 60/195,196  
PRIOR FILING DATE: 2000-04-07  
PRIOR APPLICATION NUMBER: 60/254,876  
PRIOR FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 367  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-157-930-6

Query Match 14.2%; Score 257; DB 7; Length 367;  
Best Local Similarity 33.0%; Pred. No. 5.7e-16;  
Matches 59; Conservative 34; Mismatches 78; Indels 8; Gaps 2;  
Qy 30 YSIIFILGLPLNGTVLWHFWGQTKRWSGATTVLVNLMVADLLVYL-LPFLIITYSLDDRW 88  
Db 66 YLLDFILALVGNLTALWLFIRDHKSCTPANVFLMHLAVADLSCVVLPTPLVYVHFSGNHW 125  
Qy 89 PFGELCKLVHFLFYINLYGSIILLTLCISVHQLGVCHPLCSLPYRTRHAWLGTSTTWA 148  
Db 126 PFGELCKLVHFLFYINLYGSIILLTLCISADRLFAIVHPVKSLKRLRPLVLAHLACAFW 185  
Qy 149 LVVLQPLTAFSHDTYINGQMIWYDWTSE-----NFDRLFAYGIVLTLGSLFLSLL 200  
Db 186 VVAVAMAPLLVSPQTQVNTHTVVLQLYREKASHALVSLAVAFPTFFITVTCYLLII 244

RESULT 5  
US-10-995-561-713  
Sequence 713, Application US/10995561  
Publication No. US20050272054A1  
GENERAL INFORMATION:  
APPLICANT: CARGILL, Michele et al.  
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
DISORDERS AND DRUG RESPONSE, METHODS OF  
DETECTION AND USES THEREOF  
FILE OF INVENTION: CARDIOVASCULAR DISORDERS AND  
FILE REFERENCE: CL001559  
CURRENT FILING DATE: 2004-11-24  
CURRENT APPLICATION NUMBER: US/10/995,561  
NUMBER OF SEQ ID NOS: 85702  
SOFTWARE: FastSeq for Windows Version 4.0





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; FILE REFERENCE: 00325.US1
; CURRENT APPLICATION NUMBER: US/10/980,388
; CURRENT FILING DATE: 2004-11-02
; PRIOR APPLICATION NUMBER: US/09/791,932
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/184,305
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,304
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,303
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
; LENGTH: 97
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-388-92

Query Match      13.1%; Score 238; DB 6; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKVDNMTSQEGLQCFSEKQVYLSLAYSIIFFILGLPLNGTVLW 46
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Db 52 MEKVDNMTSQEGLQCFSEKQVYLSLAYSIIFFILGLPLNGTVLW 97

RESULT 13
US-10-821-234-934
; Sequence 934, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pc_seq_genes version 1.0
; SEQ ID NO 934
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-934

Query Match      12.9%; Score 234.5; DB 6; Length 485;
Best Local Similarity 33.5%; Pred. No. 8.5e-14;
Matches 56; Conservative 34; Mismatches 74; Indels 3; Gaps 2;

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Db 163 LEVPSVYTGVFVSLPLNMAIVVFLIKMKVKKPAVVMYMLHATADVLVSLVFPKISY 222
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 83 SLDDRWPFGELCKLVHFLFYINLYGSIILLTLCISVHQFLGVCHPLCSLPYRTRRWLG 142
    ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
; FILE REFERENCE: 21402-251
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 248
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; 
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 14:42:34 ; Search time 46 Seconds  
(without alignments)  
598.500 Million cell updates/sec

Title: US-10-088-726-20  
Perfect score: 1812  
Sequence: 1 MEKVDMTSQGLQCFSEK.....NKLGEHPAGRKRCPLNRSG 333

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/iaa/PCRTUS\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	429	23.7	374	2	US-09-745-842-15
2	397	21.9	328	2	US-08-513-974B-39
3	397	21.9	328	2	US-08-513-974B-371
4	397	21.9	328	2	US-09-461-436B-39
5	395.5	21.8	377	2	US-09-745-842-17
6	394.5	21.8	328	2	US-08-513-974B-56
7	394.5	21.8	328	2	US-08-513-974B-380
8	394.5	21.8	328	2	US-09-461-436B-56
9	389.5	21.5	328	2	US-08-745-842-18
10	385.5	21.3	327	2	US-08-513-974B-372
11	382.5	21.1	375	1	US-08-442-134A-2
12	382.5	21.1	375	1	US-08-444-581B-2
13	382.5	21.1	375	1	US-08-446-088A-2
14	382.5	21.1	375	1	US-08-559-524A-3
15	382.5	21.1	375	2	US-08-749-707-3
16	382.5	21.1	375	2	US-09-947-922-3
17	377	20.8	375	2	US-08-513-974B-373
18	375	20.7	365	2	US-09-745-842-16
19	375	20.7	365	2	US-09-077-173D-2
20	372.5	20.6	374	2	US-09-102-710B-3
21	370.5	20.4	328	2	US-08-459-046-2
22	370.5	20.4	328	2	US-09-102-710B-2
23	348	19.2	362	2	US-08-513-974B-374
24	336	18.5	373	1	US-09-745-842-14
25	334.5	18.5	373	1	US-08-559-524A-4
26	334.5	18.5	373	2	US-08-749-707-4
27	334.5	18.5	373	2	US-09-947-922-4

28	283.5	15.6	337	2	US-10-314-048A-28	Sequence 28, Appl
29	282.5	15.6	302	1	US-08-467-948A-30	Sequence 30, Appl
30	282.5	15.6	302	2	US-08-467-947A-30	Sequence 30, Appl
31	281.5	15.5	344	1	US-08-467-948A-8	Sequence 8, Appl
32	281.5	15.5	344	2	US-08-467-947A-8	Sequence 8, Appl
33	263.5	14.5	370	2	US-08-781-250-2	Sequence 2, Appl
34	257	14.2	339	1	US-08-153-848-44	Sequence 44, Appl
35	257	14.2	339	1	US-08-812-871-3	Sequence 3, Appl
36	257	14.2	339	2	US-09-299-843A-44	Sequence 44, Appl
37	257	14.2	339	2	US-09-088-337B-44	Sequence 44, Appl
38	257	14.2	339	2	US-09-170-496D-32	Sequence 32, Appl
39	257	14.2	339	2	US-09-170-496D-182	Sequence 182, App
40	257	14.2	339	4	PCT-US93-11153-44	Sequence 44, Appl
41	257	14.2	339	4	PCT-US95-07180-2	Sequence 2, Appl
42	254	14.0	395	1	US-08-097-938-2	Sequence 2, Appl
43	254	14.0	395	1	US-08-097-938-5	Sequence 5, Appl
44	254	14.0	395	1	US-08-476-000-2	Sequence 2, Appl
45	254	14.0	395	1	US-08-476-000-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-09-745-842-15  
; Sequence 15, Application US/09745842  
; Patent No. 6762029  
; GENERAL INFORMATION:  
; APPLICANT: Conley, Pamela B.  
; APPLICANT: Jantzen, Hans-Michael  
; APPLICANT: Ramakrishnan-DuBridge, Vanitha  
; APPLICANT: Julius David  
; APPLICANT: Hollopetter, Gunter  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: P2Y12 Receptor  
; FILE REFERENCE: 44481-5053-US  
; CURRENT APPLICATION NUMBER: US/09/745,842  
; CURRENT FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US 60/171,622  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 374  
; TYPE: PRT  
; ORGANISM: Meleagris gallopavo  
; FEATURE:  
; OTHER INFORMATION: Turkey P2Y nucleotide receptor; tp2ynovel  
US-09-745-842-15

Query Match	23.7%	Score 429;	DB 2;	Length 374;
Best Local Similarity	40.8%;	Pred. No. 2.2e-30;		
Matches	82;	Conservative	40;	Mismatches 71;
				Indels 8;
				Gaps 3;
QY	8	TSQSGQLQCFSEKQVVL	SLAYSII	FTLGLPLNGT
DB	26	TAAEAACVFNEEFK	ILLPI	SGIVFVGLPLNSWAWIFVSRMRPNNA
QY	68	ADLLVYL-LPFLI	ITYISLDD	RWPFGEELCKLVHFLFYINLYSGIS
DB	86	SDTLVFS	SLPTLVVYAD	RNNWPFGEKVFCKIVFLFYANLYSSIL
QY	127	PLCSLP	TRRRHAWLGT	STTVALVQLPLTASHTDYINGQMTWYD
DB	146	FIRSLK	WVKTTHARL	ICVGVWLVVITICLIPNLFI
QY	187	YGIVL	TLTGSLGLLGH	FGVLF 207
DB	206	YS-----	SSIMALL--	FGIPP 219

RESULT 2  
US-08-513-974B-39





APPLICATION NUMBER: JP 7-007177  
FILING DATE: 20-JAN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-326611  
FILING DATE: 28-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-270017  
FILING DATE: 02-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236357  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-236356  
FILING DATE: 30-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189274  
FILING DATE: 11-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189273  
FILING DATE: 11-AUG-1945  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Resnick, David S.  
REGISTRATION NUMBER: 34,235  
REFERENCE/DOCKET NUMBER: 45753  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
INFORMATION FOR SEQ ID NO: 371:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 328 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-513-974B-371

Query Match 21.9%; Score 397; DB 2; Length 328;  
Best Local Similarity 31.9%; Pred. No. 1.4e-27;  
Matches 106; Conservative 55; Mismatches 137; Indels 34; Gaps 9;  
Qy 1 MEKVDMTSQBQGL----CFSEKVKQVYLSLAYSIIFILGPLNGTVLHFWGQTKRWS 56  
Db 1 MEQ-DNGTIQAPGLPPTTCVREDFKRLLLTPVSVLVGLPLNICVIAICASRRLLT 59  
Qy 57 CATTYVNLVADLLYVL-LPFLIITYSLDDRPFGLLCKLVHFLFYINLYGSILLTC 115  
Db 60 RSAVYTLNLADLWYACSLPLLIYNYARGDHPWPGDLACRFVRFLFYANLHGSILFLTC 119  
Qy 116 ISVHQFLGVCHPLCSLPYR-TRRHAWLGTSTTVALVVLQLPTLAFSHTDYINGOMIWD 174  
Db 120 ISFORYLGICHLASWHKRGRRAAWVGVVWLTAVTAQCLPTAVFAATGQRNRTVCYD 179  
Qy 175 MTSQENFRLFAYGVLTLGSLF-----SLLGHFGVLTDDGEPDOARGEHEDRHSQSP 230  
Db 180 LSPPLSTRYLPYGNALTVIGFLPFIALACYCMARRLCRODGPAGVQAQERSKAR 239  
Qy 231 VHPDHTGVWPLPLFCALPYHSLLLPHLL-SAFSGLPALDGSQGLQDMEAGCEQOL 289  
Db 240 M-----AVVAAVFAISLPHITKTAYLAVRSTPGVSCPVLFTFAAAYKGR 287  
Qy 290 PQPS-----PVLSP-----KGGKRVRLLOKL 311  
Db 288 PFASVNSVLDPLILFYFTQOKFRRQPHDLQL 319

RESULT 4  
US-09-461-436B-39  
Sequence 39, Application US/09461436B  
Patent No. 6538107  
GENERAL INFORMATION:  
APPLICANT: Shuji Hinuma

Yasuaki Ito  
Ryo Fujii  
TITLE OF INVENTION: G Protein Coupled Receptor Protein,  
Production, And Use Thereof  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Edwards & Angell, LLP  
STREET: 101 Federal Street  
CITY: BOSTON  
STATE: MA  
COUNTRY: USA  
ZIP: 02209  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/461,436B  
FILING DATE: 14-Dec-1999  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/513,974  
FILING DATE: 14-SEP-1995  
APPLICATION NUMBER: PCT/JP95/01599  
FILING DATE: 10-AUG-1995  
APPLICATION NUMBER: 7-093989  
FILING DATE: 19-APR-1995  
APPLICATION NUMBER: 7-057186  
FILING DATE: 16-MAR-1995  
APPLICATION NUMBER: 7-007177  
FILING DATE: 20-JAN-1995  
APPLICATION NUMBER: 6-326611  
FILING DATE: 28-DEC-1994  
APPLICATION NUMBER: 6-270017  
FILING DATE: 02-NOV-1994  
APPLICATION NUMBER: 6-236357  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-236356  
FILING DATE: 30-SEP-1994  
APPLICATION NUMBER: 6-189274  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189273  
FILING DATE: 11-AUG-1994  
APPLICATION NUMBER: 6-189272  
FILING DATE: 11-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: CONLIN, DAVID G.  
REGISTRATION NUMBER: <Unknown>  
REFERENCE/DOCKET NUMBER: 45753 DIV2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-439-4444  
TELEFAX: 617-439-4170  
INFORMATION FOR SEQ ID NO: 39:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 328 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 39:  
US-09-461-436B-39

Query Match 21.9%; Score 397; DB 2; Length 328;  
Best Local Similarity 31.9%; Pred. No. 1.4e-27;  
Matches 106; Conservative 55; Mismatches 137; Indels 34; Gaps 9;  
Qy 1 MEKVDMTSQBQGL----CFSEKVKQVYLSLAYSIIFILGPLNGTVLHFWGQTKRWS 56  
Db 1 MEQ-DNGTIQAPGLPPTTCVREDFKRLLLTPVSVLVGLPLNICVIAICASRRLLT 59  
Qy 57 CATTYVNLVADLLYVL-LPFLIITYSLDDRPFGLLCKLVHFLFYINLYGSILLTC 115

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Db 60 R5AVYTLNLAALMAYCSLPLLIYNYARGDHWPFGLACRFVRFLEYANLHGSILFLTC 119
Qy 116 ISVHOFILGVCHPLCSLPYR-TRRHAWLGTSTWALVVLQLLPTLAFSHDTYINGOMTIWD 174
Db 120 ISFORYLIGICHPLASMKRGRRAAWVCGVWVLAQCLPTAFVAATGQIRNRVTCYD 179
Qy 175 MTSQENFDRLPAYGIVLTLSGFL-----SLLGHFGVLTGQEPDQARGEPEHEDRQHSQ 230
Db 180 LSPILSTRYLFYGMATLVIGFLPFIALACYCRMARRLCRODGPAGPAQERRSKAAR 239
Qy 231 VHPDPTGVWPLHPLFCALPYHSLLLPHLL-SAFSGLEPALDQSQGLQDMEASGECEQL 289
Db 240 M-----AVVAAVFAISFLPHITKATYLAVRSTPGVSCPLETFAAAYGTR 287
Qy 290 PQPS-----PVLSPF-----KGGKNVRRLQKL 311
Db 288 PFASVNSVLDPLFYFTQOKFRQPHDLQRL 319

RESULT 5
US-09-745-842-17
; Sequence 17, Application US/09745842
; Patent No. 6762029
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; APPLICANT: Ramakrishnan-Dubridge, Vanitha
; APPLICANT: Julius, David
; APPLICANT: Holloper, Gunter
; APPLICANT: COR Therapeutics, Inc.
; TITLE OF INVENTION: P2Y12 Receptor
; FILE REFERENCE: 44481-5053-US
; CURRENT APPLICATION NUMBER: US/09/745,842
; CURRENT FILING DATE: 2000-12-26
; PRIOR APPLICATION NUMBER: US 60/171,622
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 17
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: P2Y2 purinergic receptor; p2ur
US-09-745-842-17

Query Match 21.8%; Score 395.5; DB 2; Length 377;
Best Local Similarity 33.0%; Pred. No. 2.2e-27;
Matches 118; Conservative 41; Mismatches 118; Indels 81; Gaps 13;

Qy 15 COPSEKYQVLSIAYSIIFILGPLNGTVLWHPWGQTKRWSGATTVLNLVMDLLYL 74
Db 25 CRFNEDEPKVLLPVSYGVVGLCLNAVALYIFLCRLKTNASTTYMFLHVAUSDALYAA 84
Qy 75 -LPELIITYSLDDWRPGEGLCKLVHFLFYNYLNGSILLTCTISVHQFLGVCHPLCSLPY 133
Db 85 SLPLLVYYARGDHWPFSTVLCKLVRLFTLYNLYCSILFTCTISVHRCGLGVLRSLRW 144
Qy 134 RTRRHAWLGTSTWALVVLQLLPTLAFSHDTYINGOMIWDMTSOENFDRLPAYGIVLTL 193
Db 145 GRARYARVAGAVVVLACQAPVLYFVTTISARGRTVCHDTSAPELFSRFVAYSSVM-- 202
Qy 194 SGFLSLGLGHFGVLF-----TDGOEPDQARGEPEHEDRQHSQVHP 233
Db 203 ---LGLL--FAVPAVILVCVLMARLLKPAYGTSG-----GLPRAKRKSVRT--- 246
Qy 234 DHPTGVWPLHPLF--CALPYH-----SLLPLPHLLSAPS-----GLPALDGSQC 276
Db 247 -----IAVLAVFALCFLPFHVTHTLYSFRSLDLSCHTLNAINMAYKVRPLASANS- 300
Qy 277 LQDMEASGECEQLPQPSFVLSFKGKNVRRLQKLQKLGHPA--GRKRCPCGLNRS 332
Db 301 -----LDPVLYFLAGRLVRFARDAKP-PTGPSATPARREL-GLRS 341
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RESULT 6
US-08-513-974B-56
; Sequence 56, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiko
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1945
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S.
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 45753
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 56:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 328 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-513-974B-56

Query Match      21.8%; Score 394.5; DB 2; Length 328;
Best Local Similarity 33.0%; Pred. No. 2.3e-27;
Matches 109; Conservative 42; Mismatches 142; Indels 37; Gaps 9;

Qy 5 DMNTSQEQL-----CQFSEKYKQVYLSLAYSIIFILGLPLNGTVMHFWGQTKRWSATT 60
Db 4 DNGTQALGLPPTTCVYRENFKQLLPVYSAVLAAGLPINICVITQICTSRALTRAV 63

Qy 61 YLVNLMVADLLYL-LPFLIITYSLDDRWPFGECLKLVHFLFYINLYGSILLTCTISVH 119
Db 64 YTLNALADLLYACSLPLLIYNYAQGDHWPFGDFACRLVRFYANLHGSILFTLCISFQ 123

Qy 120 QFLGVCHPLCSLPYR-TRHAWLGTSITWALVVLQLLPTLAFSHTDYINGQM1WYDMSQ 178
Db 124 RYLGIHPLAPWHRGGRRAAWLCVTVWLAVTTCQLPTAIFATGIQRNRTVCYDLSP 183

Qy 179 ENFDRLFAYGIVLTLSGFL-----SLLGHFVGLFTDQGEPPDQARGEPHEDRQHSQVHPD 234
Db 184 ALATHYMPYGWALTIVIGFLLPFAALLACYCLAC-----RLCRDGGPAEPVAQ 231

Qy 235 HPTGVWPLHPLFCALPYHSLLLPHLL-SAFSGLPALDGSQGLQDMEASGECEQLPOP- 292
Db 232 ERRGKAARMVAVVAFAISFLPHITKTAYLAVGSTPGVCTV--LEAFAAAYKGRTPF 289

Qy 293 -----SPVLSF-----KGGKNRVLLQKL 311
Db 290 ASANSVLDPILFYFTQKKFRRRPHELLQKL 319

RESULT 7
US-08-513-974B-380
; Sequence 380, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinzma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ontaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
```



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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 372:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 327 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-513-9748-372

Query Match 21.3%; Score 385.5; DB 2; Length 327;
Best Local Similarity 40.9%; Pred. NO. 1.4e-26;
Matches 83; Conservative 32; Mismatches 81; Indels 7; Gaps 4;

QY 1 MEKVDNMTSQEQL-----QFSSKYQKVLSLAYSIIFILGLPLNGTGLVLFHFMGQTKRWS 56
Db 1 MEQ-DNGTTIQAGELPPTTCVYREDFRLLLTTPYSVVVVGLEPLNICVIAQICASRRTLT 59

QY 57 CATTYLVNLMVADLLXVL-LPFLIITYSLDDRPFGBELCKLVHFLFYINLYGSILLTLC 115
Db 60 RSAVYTLNLALADLMYACSLPLLIYNYARCDDHWPFGDLACFRVRFYANLHGSILFLTC 119

QY 116 ISVHQFLGVCHPLCSLPYR-TRRHANLGTSTTVALVVLQLPLTFLAFSHDTYINGQMILWYD 174
Db 120 ISFQYLGICHPPLASHKHGGRRAAVVCGVVMVAVTAQCLRTAVFAATGIQRNRTVCYD 179

QY 175 MTSQENFDRLEAFYGVILTLGGFL 197
Db 180 LSPILSTRYLPYGMALTVIGFL 202

RESULT 11
US-08-442-134A-2
; Sequence 2, Application US/08442134A
; Patent No. 5596088
; GENERAL INFORMATION:
; APPLICANT: Boucher, Richard C.
; APPLICANT: Weisman, Gary A.
; APPLICANT: Turner, John T.
; APPLICANT: Harden, Thomas K.
; APPLICANT: Parr, Claude E.
; APPLICANT: Sullivan, Daniel M.
; APPLICANT: Erb, Laura
; APPLICANT: Lustig, Kevin D.
; TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
; TITLE OF INVENTION: Null Cells Expressing P2U Receptors
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bell, Seltzer, Park & Gibson
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5596088th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,134A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 375 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-442-134A-2
;
Query Match      21.1%; Score 382.5; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

QY 15 CQSEKXKQVYLSLAYSIIFILGPIPLNGTVLWHFWGQTKWSCATTYLVNLMVADLLIYVL 74
DB 25 CRNFEDFKYLLPVSYGVWCVLGLCLNAVGLYIFLCRLKTNASTTTFMFLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPGELCKLVHFLFYINLYGSILLTLCISVHOFGLGVCHPLCSLPY 133
DB 85 SLPLLVYYARGDHWPFSTVLCKLVRFYTNLYCSILFLTCISVHRCGLGVRLRSLRW 144
QY 134 RTRRHWLGTSTTVALVQLPLTAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 193
DB 145 GRARYARRVAGAVWVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLILGHGVLPF-----TDQEPDQARGEHEDRQHSQVHP 233
DB 202 ---LGLL--FAVPFAVILVCYLMARLLKPAYGTSG-----GLPRAKRKSVRT--- 245
QY 234 DHPTGVNPLHPLF--CALPYH-----SLLPHHLISAFSGLPALDGSQGLQDME 281
DB 246 -----IAVLAVALFALCFPHVTRTYLSPRSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPOPSVLPSPFKGKNRVLLQKLRQNKLGHEHPA-GRKRCPLNRS 332
DB 294 SANSC-----LDPVLYFLAQRLVRFAADAKP-PTGSPATPARRTLGLRRS 339

RESULT 12
US-08-444-581B-2
; Sequence 2, Application US/08444581B
; Patent No. 5607836
; GENERAL INFORMATION:
;   APPLICANT: Boucher, Richard C.
;   APPLICANT: Weisman, Gary A.
;   APPLICANT: Turner, John T.
;   APPLICANT: Harden, Thomas K.
;   APPLICANT: Parr, Claude E.
;   APPLICANT: Sullivan, Daniel M.
;   APPLICANT: Erb, Laura
;   APPLICANT: Lustig, Kevin D.
;   TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
;   TITLE OF INVENTION: Null Cells Expressing P2U Receptors
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Bell, Seltzer, Park & Gibson
;   STREET: Post Office Drawer 34009
;   CITY: Charlotte
;   STATE: No. 5607836th Carolina
;   COUNTRY: USA
;   ZIP: 28234
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   FILING DATE: 19-MAY-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION NUMBER: US 08/442,134
;   FILING DATE: 16-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Sibley, Kenneth D.

; SEQUENCE CHARACTERISTICS:
;   LENGTH: 375 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-444-581B-2
;
Query Match      21.1%; Score 382.5; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

QY 15 CQSEKXKQVYLSLAYSIIFILGPIPLNGTVLWHFWGQTKWSCATTYLVNLMVADLLIYVL 74
DB 25 CRNFEDFKYLLPVSYGVWCVLGLCLNAVGLYIFLCRLKTNASTTTFMFLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPGELCKLVHFLFYINLYGSILLTLCISVHOFGLGVCHPLCSLPY 133
DB 85 SLPLLVYYARGDHWPFSTVLCKLVRFYTNLYCSILFLTCISVHRCGLGVRLRSLRW 144
QY 134 RTRRHWLGTSTTVALVQLPLTAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 193
DB 145 GRARYARRVAGAVWVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLILGHGVLPF-----TDQEPDQARGEHEDRQHSQVHP 233
DB 202 ---LGLL--FAVPFAVILVCYLMARLLKPAYGTSG-----GLPRAKRKSVRT--- 245
QY 234 DHPTGVNPLHPLF--CALPYH-----SLLPHHLISAFSGLPALDGSQGLQDME 281
DB 246 -----IAVLAVALFALCFPHVTRTYLSPRSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPOPSVLPSPFKGKNRVLLQKLRQNKLGHEHPA-GRKRCPLNRS 332
DB 294 SANSC-----LDPVLYFLAQRLVRFAADAKP-PTGSPATPARRTLGLRRS 339

RESULT 13
US-08-446-088A-2
; Sequence 2, Application US/08446088A
; Patent No. 5691156
; GENERAL INFORMATION:
;   APPLICANT: Boucher, Richard C.
;   APPLICANT: Weisman, Gary A.
;   APPLICANT: Turner, John T.
;   APPLICANT: Harden, Thomas K.
;   APPLICANT: Parr, Claude E.
;   APPLICANT: Sullivan, Daniel M.
;   APPLICANT: Erb, Laura
;   APPLICANT: Lustig, Kevin D.
;   TITLE OF INVENTION: DNA Encoding the Human P2U Receptor and
;   TITLE OF INVENTION: Null Cells Expressing P2U Receptors
;   NUMBER OF SEQUENCES: 8
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Bell, Seltzer, Park & Gibson
;   STREET: Post Office Drawer 34009
;   CITY: Charlotte
;   STATE: No. 5691156th Carolina
;   COUNTRY: USA
;   ZIP: 28234
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patent In Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   FILING DATE: 19-MAY-1995
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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-446-088A-2

Query Match      21.1%; Score 382.5; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

QY 15 CQSEKYYQVYLSLAYSIIIFILGLPLNGTVLWHFQGTKRWSCATTYLVNLMVADLLYVL 74
DB 25 CRFNEDFKYVLLPVSYGVVGVCLNAGVLYIFLCRLKTNASTTYMFHLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQFLGVCHPLCSLPY 133
DB 85 SLPLLVYYARGDHWPFSTVLCKLVRFVLYTNLYCSILFLTCTISVHRCGLGVLRPLRSRW 144
QY 134 RTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTQENFDRLFYAGIVLTL 193
DB 145 GRARYARRVAGAVVVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLGHFGVLF-----TDGQEPDQARGEHPEDRQHSQVHP 233
DB 202 ---LGLL--FAVPAVILVCVYLMARRLLKPAYGTSG-----GLPRAKRSVRT--- 245
QY 234 DHPTGVWPLHPLF--CALPYH-----SLLLPHLLSAFSGLPALDGSQCGLQDME 281
DB 246 -----IAVLAVFALCFPFHVTRTLTYYSFRLSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPQSPVLSFKGKGNRVLQKLRQNKLGHEHPA-GRKRCPCGLNRS 332
DB 294 SANSC-----LDPVLYFLAGQLRVRFARDAKP-PTGPSFATPARTLGLRRS 339

RESULT 14
US-08-559-524A-3
; Sequence 3, Application US/08559524A
; Patent No. 5871963
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/559,524A
; FILING DATE: 15-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenneth D. Sibley
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-71C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-559-524A-3

Query Match      21.1%; Score 382.5; DB 1; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

QY 15 CQSEKYYQVYLSLAYSIIIFILGLPLNGTVLWHFQGTKRWSCATTYLVNLMVADLLYVL 74
DB 25 CRFNEDFKYVLLPVSYGVVGVCLNAGVLYIFLCRLKTNASTTYMFHLAVSDALYAA 84
QY 75 -LPFLIITYSLDDRWPFGEELCKLVHFLFYINLYGSIILLTCTISVHQFLGVCHPLCSLPY 133
DB 85 SLPLLVYYARGDHWPFSTVLCKLVRFVLYTNLYCSILFLTCTISVHRCGLGVLRPLRSRW 144
QY 134 RTRRHWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTQENFDRLFYAGIVLTL 193
DB 145 GRARYARRVAGAVVVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201
QY 194 SGFLSLGHFGVLF-----TDGQEPDQARGEHPEDRQHSQVHP 233
DB 202 ---LGLL--FAVPAVILVCVYLMARRLLKPAYGTSG-----GLPRAKRSVRT--- 245
QY 234 DHPTGVWPLHPLF--CALPYH-----SLLLPHLLSAFSGLPALDGSQCGLQDME 281
DB 246 -----IAVLAVFALCFPFHVTRTLTYYSFRLSLDLSCHTLNAIN-----MAYKVTRLA 293
QY 282 ASGCEQLPQSPVLSFKGKGNRVLQKLRQNKLGHEHPA-GRKRCPCGLNRS 332
DB 294 SANSC-----LDPVLYFLAGQLRVRFARDAKP-PTGPSFATPARTLGLRRS 339

RESULT 15
US-08-749-707-3
; Sequence 3, Application US/08749707
; Patent No. 6063582
; GENERAL INFORMATION:
; APPLICANT: Conley, Pamela B.
; APPLICANT: Jantzen, Hans-Michael
; TITLE OF INVENTION: NOVEL PURINERGIC RECEPTOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN, LEWIS & BOCKIUS LLP
; STREET: 1800 M Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036-5869
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,707
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Adler, Reid G.
; REGISTRATION NUMBER: 30,988
; REFERENCE/DOCKET NUMBER: 044481-5010-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-467-7000

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; TELEFAX: 202-467-7176
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-749-707-3

Query Match      21.1%; Score 382.5; DB 2; Length 375;
Best Local Similarity 33.0%; Pred. No. 3.2e-26;
Matches 116; Conservative 43; Mismatches 122; Indels 71; Gaps 13;

Qy 15 QFSEKQVYLSAYSIIFILGUPLNQTVLWHFWGQTKRWSGATTYLVNLMVADLLYVL 74
Db 25 CRFNEDFKYVLLPVSYGVVGVCLNAGVLYIFLCRLKTNASTTYMFHLAVSDALYAA 84

Qy 75 -LPELIITYSLDDRWPFGEELCKLVHFLFYINLYGSIILLITCISVHQFLGVCHPLCSLPY 133
Db 85 SLPLLVYYIYARGDHWPFSTVLCVLRFLFYTNLYCSILFLTCISVHRCGLGVLRFLSLRW 144

Qy 134 RTRRHAWLGTSTTVALVQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLTL 193
Db 145 GRARYARRVAGAVVVLVLAQAPVLYFVTTTS-ARGPLTCHDTSAPELFSRFVAYSSVM-- 201

Qy 194 SGFLSLIGHFGVLF-----TDGQEPDQARGEPEHEDRQHSQVHP 233
Db 202 ---LGLL--FAVPEAVILVCYVLMARRLLKPAYGTSG-----GLPRAKRSVRT---- 245

Qy 234 DHPTGVWPLHPLF--CALPYH-----SLLLPHLLSAFSGLPALDGSQCGLQDME 281
Db 246 -----IAVVLAVFALCFLPFHVTTLTYSPFRSLDLSCHTLNAIN-----MAYKVTRLA 293

Qy 282 ASGECEQLPQSPSVLSFKGKGKRVRLQLKLRQNKLGHPA-GRKRCPLNRS 332
Db 294 SANSCL-----LDPVLYFLAGORLVRFARDAKP-PTGSPATPARRTLGLRRS 339
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Searched: 6247088 seqs, 457523669 residues  
Total number of hits satisfying chosen parameters: 12494176  
Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	179	17.9	1428	7	US-10-995-561-13208
4	166.4	16.6	2693	11	US-11-136-527-3005
5	165.2	16.5	2684	11	US-11-136-527-3527
6	158.4	15.8	1945	11	US-11-136-527-1845
7	147.8	14.8	1400	11	US-11-136-527-5941
8	138	13.8	551	7	US-10-980-388-32
9	107.4	10.7	3122	11	US-11-127-877-9
10	104.2	10.4	3288	11	US-11-136-527-3178
11	99	9.9	1685	7	US-10-750-185-36071
12	99	9.9	1685	7	US-10-750-623-36071
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18	85.4	8.5	3635	11	US-11-136-527-2101
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21	82	8.2	1095	8	US-11-040-218-80

22	82	8.2	1137	8	US-11-040-218-82	Sequence 82, Appl
23	80.4	8.0	1782	11	US-11-136-527-3486	Sequence 3486, Ap
24	79.6	7.9	1116	11	US-11-136-527-2638	Sequence 2638, Ap
25	79.6	7.9	1116	11	US-11-134-811-5	Sequence 5, Appli
26	78.8	7.9	1102	7	US-10-955-054A-121	Sequence 121, App
27	78.8	7.9	1225	7	US-10-955-054A-112	Sequence 3, Appli
28	78.8	7.9	1662	11	US-11-028-922A-3	Sequence 141, App
29	78.8	7.9	8747	7	US-10-955-054A-141	Sequence 30, Appl
30	77	7.7	1523	11	US-11-127-877-30	Sequence 321, App
31	75.4	7.5	1238	7	US-10-995-561-321	Sequence 30, App
32	75.4	7.5	1498	7	US-10-995-561-320	Sequence 30, App
33	75.4	7.5	4267	11	US-11-127-877-15	Sequence 15, Appl
34	75.4	7.5	86131	7	US-10-995-561-13298	Sequence 13298, A
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36	74.4	7.4	1290	11	US-11-136-527-6553	Sequence 6553, Ap
37	73.6	7.3	1050	11	US-11-028-922A-4	Sequence 4, Appli
38	73.6	7.3	1651	11	US-11-136-527-2630	Sequence 2630, Ap
39	73	7.3	1384	11	US-11-136-527-2159	Sequence 2159, Ap
40	71.8	7.2	2955	11	US-11-136-527-2954	Sequence 2954, Ap
41	69.4	6.9	536	7	US-10-980-388-35	Sequence 35, Appl
42	69.4	6.9	1163	11	US-11-136-527-2458	Sequence 2458, Ap
43	68.8	6.9	3883	11	US-11-136-527-3673	Sequence 3673, Ap
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c 45	68.6	6.8	1224	7	US-10-750-623-40492	Sequence 40492, A

ALIGNMENTS

RESULT 1  
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; Sequence 3805, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3805  
; LENGTH: 2011  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-3805

Query Match	18.9%	Score 189.4	DB 11	Length 2011
Best Local Similarity	53.7%	Pred. No. 2.1e-40		
Matches	461	Conservative	0	Mismatches 391; Indels 7; Gaps 3
QY	43	TGCCAGTTCTCAGAGAAGTACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTT	102	
Db	556	TGTCGCTTCAACGAGGACTTCAAGTATGTGCTGCTGCCCGTCTCTATGGCGTGTGTGC	615	
QY	103	ATCTAGGGTGGCCACTAAATAGGCACTGCTTTGTGGCACTTCTTGGGGGCAACCAAGCGC	162	
Db	616	GTGCTCGGGCTGTGCTGAGAGCTGCTGCCCTCTACATCTTCTGTGGCGCTCAAGACC	675	
QY	163	TGGAGCTGTGCCACCACTATCTGGTGAACCTGATGGTGGCGGACCTCTTATGTGCTA	222	
Db	676	TGGAAAGCGCTCCACCACTATCTGTTTACCTCTGGCAGTTCTCTATCTCTACGAGCC	735	
QY	223	T---TGCCCTTCTCTCATCATCATCTCTACTAGTATGACAGTGGCCCTTCGGGAGCTG	279	
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QY	280	CTCTGCAAGCTGGTGACCTTCTCTGTCTATATCAACCTTTAGGAGCATCTCTGTCTG	339	
Db	796	CTCTGCAAGCTGGTGCGTTTCTCTTTCTACACTAACCTCTACTGAGCATCTCTCTCTC	855	

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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1095 TCTGCTTTTGTCTGTGCCCTTTTCCATCATCTCTGCTGTGTACGTCTCATGGCCCGACG 1154
Qy 640 GATCAAGCCAGAGAGAACTCATGAGGACAGGCAACACAGCCGAGCCAGGTCCATCCG 699
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1155 GCTGCTCAAAACCGGCTTATGGGACCAACAGGTCTGCTCGGGCCAAAGCTGTGGC 1214
Qy 700 GACATCTACTGTGTGGCTCTTTCACCTCTGTGTTTGTGGCCCTTCCATATCACTCG 759
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1215 CACCATCGCTTAGTACTGGCCGCTTTTGGCCCTCTGCTTCTGCTTTTCCACGTCACCCG 1274
Qy 760 CTGCTTCTACTCTACCATCTGCTTTCTGCTTCTCTCAGGACTGCCAGCTCTTGTATGGCAG 819
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1275 CACCTCTATTACTCTTCCGATCA---CTTGACCTCAGTTGGCCACACCTCTCAAGCCAT 1331
Qy 820 CAGTGTGGCTTACAAGATATGGAGGCTCTGGTGTGTGTGAGTGTGAGCAGTGCCTCAACCCAGT 879
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1332 CAACATGGCTATTAAGATCACCCGGCCACTGGCCAGCGCAACAGTGTGCTTGACCTGT 1391
Qy 880 CCTGTACTTTCTTTCAAGG 898
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1392 GCTTACTTCTCGCAGGG 1410
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## RESULT 2

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US-10-995-561-28
; Sequence 28, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-28
```

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Query Match 17.9%; Score 179; DB 7; Length 1428;
Best Local Similarity 53.8%; Pred. No. 1e-37;
Matches 479; Conservative 3; Mismatches 393; Indels 16; Gaps 5;
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Qy 42 CTGCGCATTCTCAGAGTACAGACGAGTCTACCTCTCCCTGCCCTACAGTATCATCTT 101
Db 258 CTGTGTGTGTATGAGGATTCAGTTCATCTCTGCTGCTGCTGAGCTATGAGTTGCTT 317
Qy 102 TATCTAGGGGTGCCACTTAATGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
Db 318 TGTCTGGGCTTGGCCCTTAACGCCCAACCCATATGCTCTTCACTCTTCCGCTCCGACC 377
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Qy 162 CTGAGCTGTGCCCAACCACTTATCTGTGAACTGTATGGTGGCCGACCTGCTTTATGTGCT 221
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
378 CTGGGATGCAACCGGCCACCTTACATGTTCCACCTGGCATTTGTGACACACCTTGTATGTGCT 437
Qy 222 AT---TGCCCTTCTCATCATCACTACTACTAGATGATGACAGTGGCCCTTCGGGAGCT 278
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
438 GTGCTGGCCACCTCATCTATTATGAGCCCAACACCTGGCCCTTTGGCACTGA 497
Qy 279 GCTCTGAAGCTGGTCACTTCTGCTTTATATATAAACCCTTTAGGGCAGACATCTCTGCTGCT 338
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
498 GATCTGCAAGTTGTGGCTTTCTTTTCTATTGGAACCTCTACTGCAAGTGTCTTTTCTCT 557
Qy 339 GACCTGCATCTGTGACCAAGTTCCTAGGTGTGTGCCACCACTGTGTTGCTGTGCCCTA 398
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
558 CACCTGCATCAGCGTGCACCGCTACCTGGGCATCTGCCACCCACTTCGGGCACTACGCTG 617
Qy 399 CCGGACCCGAGCATGCTGGCTGGCCGACCAAGCACTGGGCCCTTGGTGGTCTCCCA 458
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
618 GGGCCGCTCTGGCTCGCAGGCTTCTCTGCTGGCAGTTTGGTGGTCTGAGCCGCTG 677
Qy 459 GCTGCTGCCCACTCTGCTTCTCCACACGCACTACATCAATGGCCAGATGATCTGGTA 518
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
678 CCTCTGCCCAACCTGTCTTGTGTACAAACAGGACCAACCGTCTCTGTGCCA 737
Qy 519 TGACATGACGAGCAAGAGAAATTTGATCGGCTTTTGTGCTTACGGCATAGTTCTGCAATT 578
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
738 TGACACCACTCGGCTGAAGAGTTTGACCACTATGTGCACTTCAGCTCGCGGCTCATGGG 797
Qy 579 GTCTGGCTTT---CTTTCCCTCTGCTGCTATTTTGGTGTGCTATTCATGATGTGAGGAG 636
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
798 GCTGCTTTTGGGCTGGCTGCTGTGCTCTTGTGTGATGAGCTCATGGCTCTGCTG 857
Qy 637 CTTGATCAAGCCAGAGAGAACTCATGAGGACAGGCAACACAGCCGAGCCAGGTCAT 696
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
858 CTTGATCAGCCCTTG-----CCAGGCKTGCACAGTCTCTTCTCGCCTCCGCTCTCT 911
Qy 697 CCGGACATCTACTGCTGTGGCTCTTTCACCTCTGTTTGTGGCCCTTCCATATFAC 756
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
912 CCGCACRTAGCTGTGTGCTGCTCTCTTTGCTGTCTGCTGCTGCTTTTCCACATCAC 971
Qy 757 TCGCTCTTCTACTCTACCATCTGCTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGC 816
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
972 CCGCACATTTTACTCTGCGCCAGGCTTGTGGAAGCT---GACTCGGAGTACTGAACAT 1028
Qy 817 AGCCAGTGTGGCCCTACAAGATATGAGGCTCTGTGAGTGTGAGCAGCTGCTCAACCC 876
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1029 TGTCAACGTGTCTATAAAGTGAAGTCTGGCCCTGGCCAGTGGCCAAACAGCTGCTGGATCC 1088
Qy 877 AGTCTGTACTTTCTTTCAAGGGGGGCAAAATAGAGTCAAGGCTCTCTCCAG 927
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1089 TGTGCTCTACTTGC--TCACTGGGGCAAAATATCGAGCTCGAGCTCCTCTCAG 1137
```

## RESULT 3

```
US-10-995-561-13208
; Sequence 13208, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13208
; LENGTH: 13428
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13208
```

Query Match 17.9%; Score 179; DB 7; Length 13428;  
Best Local Similarity 53.8%; Pred. No. 2.5e-37;  
Matches 479; Conservative 3; Mismatches 393; Indels 16; Gaps 5;  
Qy 42 CTGCAGTTCTCAGAGAGTCAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTT 101  
Db CTGTTGGTTTGTATGAGGATTTTCAGTTTCATCTGCTGCTGTGAGCTATGACAGTTGCTT 6316  
Qy 102 TATCTAGGCTGCCACTAAATGACATGTTCTTGGCACTTCTGGGGCCAAACCAAGCG 161  
Db TGTCTGGCTTGGCCCTTAACGCCCAACCTATGCTCTTTCATCTTCGCGCTCCGACC 6376  
Qy 162 CTGAGCTGTGCCACCACTATCTGTGTGAACCTGATGTGGCCGACCTGCTTTATGTGCT 221  
Db CTGGATGCAAGGCCACCTACATGTTCCACCTGGCATTTGCAGACACCTGTATGTGCT 6436  
Qy 222 AT---TGGCCCTTCTCATATCATACCTACTACTAGATGACAGTGGCCCTTCGGGAGCT 278  
Db GTCGCTGCCACCTCATCTACTATTATGACAGCCCAACCACTGGCCCTTTTGGCACTGA 6496  
Qy 279 GCTCTGAAGTGTGCT 338  
Db GATCTGAAGTGTGCT 6556  
Qy 339 GACCTGCATCTCTGTGACCAAGTTCTCTAGGTGTGTCACCACTGTTGCTGTCCTTA 398  
Db CACTGTGATGCTGACCGCTACCTACCTGCGGCACTGCCACCACTTCGCGCACTACGCTG 6616  
Qy 399 CCGGACCGCAGGCACTGCTGGCTGGGCAACAGCACCACTGGCCCTGTGTGCTCTCCA 458  
Db GGGCGGCTCGCTCGAGGCTTCTCTGCTGGCAGTTTGGTTGTTGCTAGCGGCTG 6676  
Qy 459 GCTGCTGCCACATCTGGCTTCTCCCAACAGCACTATCAATCAATGGCAGATGATCTGGTA 518  
Db CCTCTGCCCAACCTGTTCTTGTGACAAACAGCAGCAAGGAGGACCACTGCTGTGCCA 6736  
Qy 519 TGACATGACCAAGCAAGAAATTTTGGCTGTTTGGCTTACCGGCACTGTTCTGACATT 578  
Db TGACACCACTCGGCTGAAGAGTTTGACCACTATGTGCACTTCAGCTGGCGGTCTGGG 6796  
Qy 579 GTCTGGCTTT---CTTTCCTCTTGGTCAATTTTGGTGTGCTTATTCACCTGATGTGAGG 636  
Db GCTGCTCTTTGGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6856  
Qy 637 CTTGATCAAGCAGAGAGAACCTCATGAGAGACAGGCAACACAGCCGAGCCAGGCTCAT 696  
Db CCTGTATCAGCCCTTG-----CCAGGCKCTGCACAGTCTGCTTCTGCGCTCCGCTCTCT 6910  
Qy 697 CCGGACCATCTACTGTTGTGGCTCTTACCCCTCTGTTTGTGGCTTCCATATCAC 756  
Db CCGCACCACTAGCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6970  
Qy 757 TCGCTCTCTTACCTCACCCTGCTTCTGCTTCTCAGGACTGCCAGCTCTTGTATGGC 816  
Db CCGCACCACTTACTACCTGGCCAGGCTGTTGGAAGCT---GACTGGCCGAGTACTGAACAT 7027  
Qy 817 AGCCAGTGTGCTTACAGATATGAGGCTCTCTGAGTGTGAGAGCTGCTCTCAACCC 876  
Db TGTCAAGCTGTCTATAAAGTGACTCGGCCCTGGCCAGTGCCAAGCTGCTCTGGATCC 7087  
Qy 877 AGTCTGTACTTCTTTCAGGGGGGCAAAATATAGTCAAGCTCTCTCCAG 927  
Db TGTGCTCTACTTGC---TCACTGGGGAACAAATATCGAGTCAAGCTCCRTCAAG 7136

RESULT 4  
US-11-136-527-3005  
; Sequence 3005, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M

; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3005  
; LENGTH: 2693  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; US-11-136-527-3005  
Query Match 16.6%; Score 166.4; DB 11; Length 2693;  
Best Local Similarity 53.5%; Pred. No. 2.9e-34;  
Matches 483; Conservative 1; Mismatches 402; Indels 16; Gaps 6;  
Qy 31 GAACAAGTCTCTGCCAGTTCTCAGAGAAGTACAGAAGTCTACCTCTCCCTGGCCTAC 90  
Db GGAGATGGTGTATGTAGTTTAAATGAGAGTTCAAGTTTCATCTCTGTTGCCCTATGAGCTAT 1480  
Qy 91 AGTATCATCTTTATCTCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGC 150  
Db GCAGTTGTGTTTGTCTGGGCTGGCCCTCAATGCTCAACCTCTGGCTGTCTCTCTTC 1540  
Qy 151 CAAACCAAGCGCTGGAGCTGTGCCACCACTATCTGTGAACCTGATGGTGGCCGACCTG 210  
Db CGCCTTTCGACCTCTGGAGATCAACAGCACCTACATGTTCCACCTGGCATTTGTTCAGACAC 1600  
Qy 211 CTTTATGTGCTAT---TGCCCTCTCTCATCATCACTACTACTAGATGACAGTGGGCC 267  
Db TTGTATGTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1660  
Qy 268 TTGGGAGAGTGTCTGCAAGCTGGTGCATCTCTGTTCTATATCAACCTTTACGGCAGC 327  
Db TTTGGCACTGGCCCTTTCGAAAGTTTGTCCGCTTCTCTCTTATTTGGAACCTCTACTAGT 1720  
Qy 328 ATCTGTCTGTGACCTGCATCTCTGTGCACAGTTCCTAGTGTGTGCCACCACTGTGT 387  
Db GTCTCTTCTCTACCTGCATCTGCTGACCGATACCTGCTGGGTATCTGCCACCACTGGG 1780  
Qy 388 TCGTGTCCCTACCGGACCCGCGAGCATGCTGGCTGGGCAACAGCACCACTGGGCCCTG 447  
Db GCAATCGCTGGGGCGCCCTCGATTTGCAAGCTTCTCTGCTGGGTGTTGTTGGTA 1840  
Qy 448 GTGTCTCTCAGCTGTGTGCCACATGCGCTTCTCCACAGGACTACATCAATGGCCAG 507  
Db GTAGTGGCTGCTGCTGCGCAATCTTTCTTTGTGACAAACCAATGCAATGGAACTACC 1900  
Qy 508 ATGATCTGGTATGACATGACCGCAGAGAAATTTTGTATCGGCTTTTGTGCTACGGCATA 567  
Db ATCTGTGCAATGACACTACTCTGCGAGAGAGTTTACCACTACGCTTACTCTCAGTTCTG 1960  
Qy 568 GTTCTGACATTTGTCTGGCTTT---CTTTCCCTCTCTGCTCATTTTGTGTGTCTATTCACTG 625  
Db GCAGTCACTGTGTGCTCTTTGTTGCTTCTCTGATCACCCTGGTCTGCTATGGACTC 2020  
Qy 626 ATGCTCAGGAGCTGTATCAAGCCAGAGAGAACTCATAGGACAGCAAGCAACAGCCGGA 685  
Db ATGGCCCGGCTGTATGACCTTTG---CCAGGAGCTGGACAGTCA---TCTTCTCGG 2074  
Qy 686 GCCAGGTGCATCCGGACCATCTACTGTTGTGGCTTTCACCTCTGTTTGTGGCC 745  
Db CTCTGTTCCCTGCGTACCATTTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2134  
Qy 746 TTCCATATCACTGCTCTCTTCTACCTCACTCTGCTTTTCTGCTTTCTCAGGACTGCGAG 805  
Db TTCCATATCACTGCTCTCTTCTACCTCACTCTGCTTTTCTGCTTTCTCAGGACTGCGAG 2191  
Qy 806 CTCTTGTAGGAGCAGCTGTGGCTTACAGATATGAGGCTCTGTGGTGTGAGTGAGCAGC 865  
Db GTGCTGAACATTTGTAATGTGGTTTACAGGTGACTCGACCCCTGGCCAGTGTCTAATAGC 2251

Qy 866 TGCTCAACCCAGTCTCTGTTACTTCTTCAAGGGGGCAAAAATAGAGTCAGGCTCTCC 925  
Db 2252 TGTCTGATCCAGTCTCTA--TCTCTTCAAGGGGGCAAGATATCGAAACAGCTCCAGC 2309  
Qy 926 AG 927  
Db 2310 AG 2311  
RESULT 5  
US-11-136-527-3527  
; Sequence 3527, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 60/574,294  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3527  
; LENGTH: 2684  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-3527

Query Match 16.5%; Score 165.2; DB 11; Length 2684;  
Best Local Similarity 53.5%; Pred. No. 6.1e-34;  
Matches 483; Conservative 0; Mismatches 403; Indels 16; Gaps 6;  
Qy 31 GAACAAGTCTCTCCAGTCTCTCAGAGAAGTACAAAGTCTACCTCTCCCTGGCCTAC 90  
Db 1412 GGAGATGGTATTTAGTATTTATGAGAGTTCAAGTTCACTCTGTTGCCATGAGCTAT 1471  
Qy 91 AGTATCATCTTTATCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGC 150  
Db 1472 GCAGTTGTGTGTGGCTGGCCCTCAATGCTCAACCCCTCTGGCTTCTCTTC 1531  
Qy 151 CAACCAAGCGCTGGAGCTGGCCACCACCTATCTGTGTAACCTGATGGTGGCGAGCTG 210  
Db 1532 CGCCTTCGACCTGGGATGCAACGACCCCTACATGTTCCACCTGGCAATGTCCAGACCC 1591  
Qy 211 CTTTATGTGTAT--TGCCCTTCTCATCATCACTACTCACTAGATGACAGTGGCCC 267  
Db 1592 TTGTATGTGTGTCACTGCCACCCTCGTCTACTATGTTGGCAGAAACCACTGGCCC 1651  
Qy 268 TTCGGGAGCTGTCTGCAAGCTGGTGCACTTCTCTGTATATCAACCTTTACGGCAGC 327  
Db 1652 TTTGGCACTGGCTTTGCAAGTTGTCCGCTTCTCTCTATTTGGAACCTCTACTGTAGT 1711  
Qy 328 ATCTGCTGTGCACTGTGATCTGTGTGACACAGTTCTTAGTGTGTGGCCACCACTGTGT 387  
Db 1712 GTCTCTTTCTCACTGATGATGTGTCACGATACCTGGATATCTGCCACCACTCGG 1771  
Qy 388 TCCTGCTCTACCGACCCGACGATGCTGGCTGGCGGACCAACCACTGGCCCTG 447  
Db 1772 GCAATCGCTGGGGCCGCTCGATTTGCAAGCCCTCTCTGCTGGGTGTGTGGTA 1831  
Qy 448 GTGTCTCTCCAGTGTCTGCCACACTGGCCCTTCTCCACACGGAAGTCAATGGCCAG 507  
Db 1832 GTAGCTGCTGCTCGTGGCCCAATCTTCTTTGTGACAACTATGCAATGGAACTACC 1891  
Qy 508 ATGATCTGGTATGATGATGACAGCAAGAGATTTTGTATGGCTTTTGTGCTACGGGATA 567  
Db 1892 ATCTGTGCCATGACACTACTCTGCCAGAGAGTTTGACCACTACGCTCTACTTCAGTTCG 1951  
Qy 568 GTTCTGATATGTCTGGCTTT--CTTTCCCTCTCTGGTCAATTTTGGTGTGCTATTCACTG 625

Db 1952 GCAGTCATGTGTGCTCTTGTGGTTCCTTGTATCACCCTGGTCTGCTATGGACTC 2011  
Qy 626 ATGGTCAGGAGCTGTATCAAGCCAGAGAGAACTCATGAGGACAGGCAACACAGCCCGA 685  
Db 2012 ATGGCCCGGCGACTGTATCGACCTTTG---CCAGGAGCTGGACAGTCA--TCTTCTCGG 2065  
Qy 686 GCCAGGTCCATCGGACCACTCTACTGGTGTGTGGCTCTTCACTCTCTGTTTGTGGCC 745  
Db 2066 CTCGGTTCCCTCGTACCAATGTCTGTGGTGTGCTGCTGTCTCTCTGCTGCTGCT 2125  
Qy 746 TTCATATCACTCGCTCTCTTCTACCTCACCATCTGCTTTCTGCTTTCTCAGGACTGCCAG 805  
Db 2126 TTCCATCATCCCGCACAATTTATTACCAGGCAAGACTGTTGCAAGCT---GACTGTCTAT 2182  
Qy 806 CTCTTGATGGCAGCCAGTGTGGCTCAAGATATGAGAGGCTCTGTGTGATGTGAGCAGC 865  
Db 2183 GTGCTGAACATTTGCAATGTGTTTACAAGGTGACTCGACCCCTGGCCAGTGTCTAATAGC 2242  
Qy 866 TGCTCAACCCAGTCTGTACTTTCTTCAAGGGGGCAAAAATAGAGTCAGGCTCTCTCC 925  
Db 2243 TGTCTTGATCCAGTGTCTTA--TCTCTTCAAGGGGGCAAGTATCGAAACAGCTCCAGC 2300  
Qy 926 AG 927  
Db 2301 AG 2302

## RESULT 6

US-11-136-527-1845  
; Sequence 1845, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1845  
; LENGTH: 1945  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-1845

Query Match 15.8%; Score 158.4; DB 11; Length 1945;  
Best Local Similarity 51.2%; Pred. No. 3.4e-32;  
Matches 437; Conservative 4; Mismatches 405; Indels 8; Gaps 3;  
Qy 42 CTGCCAGTCTCAGAGAAGTACAAAGTCTTACCTCTCCCTGGCCTTACAGTATCATCTT 101  
Db 490 CTGGCTACCGTGAGGATTTCAAGCGACTGTCTACTACCCCGAGTTTACTCAGTGTGCT 549  
Qy 102 TATCTAGGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG 161  
Db 550 GGTGTGGCTGCCACTGAAACGTCTGTGTATCGCCAGATATCGCATCCCGCCGAC 609  
Qy 162 CTGGAGCTGGCCACCACCTATCTGTGTAACCTGATGGTGGCCGACCTGCTTTATGTGCT 221  
Db 610 CTTGACCCGTTCCGCTGTGTACACCCCTGAACTTTGGCACTGGCGACCTGCTGTATGCTG 669  
Qy 222 AT---TGCCCTTCTCATCATCACTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCT 278  
Db 670 TTCACTGCCCTTACTTATCTATACTACGACAGGGGACCACTGGCCCTTCGGAGACCT 729  
Qy 279 GCTCTGAAGCTGGTGCATCTTCTGTTCTATATCAACCTTTTACGCAAGCATCTCTGTGCT 338  
Db 730 TGGCTGGCCGCTGGTACGCTTCTCTTCTATGCAACCTTACAGCGGACGATCTCTGTTCCT 789  
Qy 339 GACCTGCATCTCTGTGACCACTTCTAGTGTGTGCCACCACCTGCTGTGCTGCTGCTA 398

Db 790 CACCTGCAATAGCTTCCAGGATACCTAGGCAATCTGCCATCCCTTGGCCCTCGCAAA 849  
Qy 399 CC---GGACCCGAGGATGCTGGCTGGGACACAGACACCTGGGCCCTGGTGTCT 455  
Db 850 GCGTGGAGGTGCGCGTCTGCTGGGTGGTATGAGAGTCGTTGGCTGGTGTGACAGC 909  
Qy 456 CCAGCTGTCGCCACACCTGCTTCTCCCAACAGGATACATCAATGAGCCAGATGATCTG 515  
Db 910 CCAGTGTGCTGCCACAGAGCTTCTGGCCGACAGGGGATCCAGGCAACCCGATGCTG 969  
Qy 516 GTATGACATGACAGCCAGAGAAATTTTGAATGCGCTTTTTCCTACGSCATAGTTCTGAC 575  
Db 970 CTAGACCTGAGCCACCCATCTGTCCACCCGCTACCTGCGATGSCATGGCCCTCAC 1029  
Qy 576 ATTGTCTGGCT--TTCCTTCCCTCCTGGTCAATTTTGTGTGCTATTCACTGATGCTGAG 633  
Db 1030 GGTATCGGCTTCTTGTCTTCCCTTACAGCCTTACTTGGCCTGCTACTGTGCTATGGCCG 1089  
Qy 634 GAGCTGATCAAGCCAGAGGAACTCTCATGAGGACAGCAACAGCCCGAGCCAGCTC 693  
Db 1090 CGCCTGTGTGCGCAGGATGCGCAGAGTCTGTGGCCCAAGAGCTCCAGCAAGGC 1149  
Qy 694 CATCGGACCATCTACTGTGTGTGGCTCTTACCCCTCTGTGTGTGGCTTCCCATAT 753  
Db 1150 GGCCGATGCTGTGCTGGTAGCAGCTGTCTTTGTTATCAGCTTCTGCTTCCCAT 1209  
Qy 754 CACTGCTCTCTTACCTACCATCTGCTTCTGCTTCTCAGAGCTGCGAGCTCTTGAT 813  
Db 1210 CACCAAGACAGCTACTTGGCTGTGCTTCCAGCCCGGCTCTCTTGGCCGCTACTGGA 1269  
Qy 814 GCGAGCAGCTGCGCTACAGATATGAGGCTCTGTGTGAGTGTGAGCAGCTGCCTCAA 873  
Db 1270 GACCTTCTGCTGAGCTTACAAAGGACCCSRMKGCCAGTGCTTAACAGCTTCTGGA 1329  
Qy 874 CCCAGTCTCTACT 887  
Db 1330 CCCTATCTCTCT 1343

## RESULT 7

US-11-136-527-5941  
; Sequence 5941, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 5941  
; LENGTH: 1400  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-5941

Query Match 14.8%; Score 147.8; DB 11; Length 1400;  
Best Local Similarity 51.5%; Pred. No. 1.9e-29;  
Matches 406; Conservative 4; Mismatches 371; Indels 8; Gaps 3;

Qy 107 TAGGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGA 166  
Db 10 TCGGCTGCCACTGAACCTGTGTGTCATCGCCAGATATGCGATCCCGCCGACCTGGA 69  
Qy 167 GCTGTGCCACCACTTATCTGTGTGAACCTGTGTGGCGGACCTGTTTATG---TGCTAT 223  
Db 70 CCGCTTCGCTGTGTACACCCCTGAACCTTGGCACTGGCGGACCTGCTGTATGCTGTTCCAC 129

Qy 224 TGCCCTTCTCATCATCACCTACTCACTAGATGACAGGTGGCCCTTGGGAGAGCTGTCT 283  
Db 130 TGCCCTTACTTATCTATTAATCACTGCGCAGAGGGGACCACTGGCCCTTGGAGACCTTGCCT 189  
Qy 284 GCAAGCTGTGTGCACTCTCTGTCTTATCAACCTTTTACGGCAGCATCTCTGTGTGACCT 343  
Db 190 GCGCCTTGGTAGCTTCTCTTCTATGCAACCTTACAGCGCAGCATCTCTTCTCTCACT 249  
Qy 344 GCATCTGTGTGCAACAGTCTCTAGGTGTGTGCGCACCCACCTGTGTGTGCTGCGCTACC--- 400  
Db 250 GCATAGCTTCCAGCATACCTAGGCATCTGCGCATCTGCGCCCTTGGCCCTTGGCAAGCGTG 309  
Qy 401 GGACCCGAGGATGCTGCTGGGCGCACAGCACCTGGGCGCTGTGTGCTCTCCAGC 460  
Db 310 GAGTCTGCGGTGCTGCTTGGGTGATGTGAGTCTGTTGGCTGGTGTGACAGCCAGT 369  
Qy 461 TGCTGCCACACTGGCTTCTCCACAGGACTATCAATGCGCAGATGATCTGTGTATG 520  
Db 370 GCCTGCCACAGCAGTCTTTCGCCCAAGGCACTCCAGCGCAACCGCACTCTCTGCTACG 429  
Qy 521 ACATGACAGCCAGAGAAATTTTGTATGGCTTTTGGCTAGCGCATAGTTCTGACATGT 580  
Db 430 ACCTGAGCCCAACCATCTCTGTCACCCGCTACCTGCGGTATGGCATGGCCCTCACGGTCA 489  
Qy 581 CTGGCTT--TCTTTCCCTCTTGTGTGCTATTTGGTGTGCTATTCACTGATGTGAGGAGCC 638  
Db 490 TCGGCTTCTGCTTCTTCTTACAGCCTTACTTGGCTTGTCTGTGCTGCGATGSCCGCGCC 549  
Qy 639 TGATCAAGCCAGAGGAACTCATGAGGACAGCAACACAGCCCGAGCCAGGTCCATCC 698  
Db 550 TGTGTCGCCAGATGGCCAGCAGTCTGTGGGCCAAGAGCGTCTGCGACGAAGGCGGCC 609  
Qy 699 GGACCATCTACTGCTGTGTGGCTCTTACCCCTCTGTTTGTGCGCTTCCATATCACTC 758  
Db 610 GTATGGCTGTGTGTAGCAGCTGTCTTGTATCAGCTTCTGCTCTTCCACATCACA 669  
Qy 759 GCTCTTCTACCTCACCATCTGCTTTCTGCTTTCTCAGGACTGCGCAGCTTGTGATGGCAG 818  
Db 670 AGACAGCTACTTGGCTGTGGCTCCAGCCCGCGGTCTCTTGGCGGTACTGGAGACT 729  
Qy 819 CCAGTGTGGCTTACAGATATGAGGCTCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAG 878  
Db 730 TCGCTGCGAGCTACAAAGGACCCSRMKGCCAGTGTCTTAACAGCGTCTTGGACCCCTA 789  
Qy 879 TCCTGTACT 887  
Db 790 TCCTCTTCT 798

## RESULT 8

US-10-980-388-32/c  
; Sequence 32, Application US/10980388  
; Publication No. US20050255490A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogeli, Gabriel  
; APPLICANT: Parodi, Luis A.  
; APPLICANT: Hiebsch, Ronald R.  
; APPLICANT: Lind, Peter  
; APPLICANT: Kaytes, Paul S.  
; APPLICANT: Huff, Valerie  
; APPLICANT: Huff, Rita M.  
; APPLICANT: Wood, Linda S.  
; TITLE OF INVENTION: Novel G Protein-Coupled Receptors Cross-Reference To Related Appl  
; FILE REFERENCE: 00325-US1  
; CURRENT APPLICATION NUMBER: US/10/980,388  
; CURRENT FILING DATE: 2004-11-02  
; PRIOR APPLICATION NUMBER: US/09/791,932  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/184,305  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,304  
; PRIOR FILING DATE: 2000-02-23  
; PRIOR APPLICATION NUMBER: 60/184,303

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; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,397
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/184,247
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/188,880
; PRIOR FILING DATE: 2000-03-13
; PRIOR APPLICATION NUMBER: 60/217,369
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/217,370
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/218,492
; PRIOR FILING DATE: 2000-07-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-980-388-32
;
Query Match      13.8%; Score 138; DB 7; Length 551;
Best Local Similarity 100.0%; Pred. No. 5.3e-27;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGAGAAGTGGACATGATATACATCACAGGAACAAGGTCTTCCAGTGTCTCAGAGAAG 60
Db      138  ATGAGAAGTGGACATGATATACATCACAGGAACAAGGTCTTCCAGTGTCTCAGAGAAG 79

Qy      61  TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTATCTTAGGCTGCCACTA 120
Db      78  TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTATCTTAGGCTGCCACTA 19

Qy      121  AATGGCACTGCTTGTGG 138
Db      18  AATGGCACTGCTTGTGG 1

RESULT 9
US-11-127-877-9
; Sequence 9, Application US/11127877
; Publication No. US20050287565A1
; GENERAL INFORMATION:
; APPLICANT: Merck, Pascal G.
; APPLICANT: Hoffmann, Marcel
; APPLICANT: Spittels, Koenraad F. F.
; APPLICANT: Laenen, Wendy
; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting
; FILE REFERENCE: P27,800-B USA
; CURRENT APPLICATION NUMBER: US/11/127,877
; PRIOR FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,352
; PRIOR FILING DATE: 2004-05-12
; PRIOR APPLICATION NUMBER: 60/603,948
; PRIOR FILING DATE: 2004-08-24
; NUMBER OF SEQ ID NOS: 590
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 3122
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-127-877-9

Query Match      10.7%; Score 107.4; DB 11; Length 3122;
Best Local Similarity 52.3%; Pred. No. 1.4e-18;
Matches 311; Conservative 0; Mismatches 276; Indels 8; Gaps 3;

Qy      72  CTACCTCTCCCTGACATGATCATCTTTATCTTAGGGCTGCCACTAAATGGCACTGT 131
Db      992  CTACCTGCGGCTGTCTACATCTTGGTATTTCATCATCGGCTTCTGGGCAACAGCGTGGC 1051
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Qy      132  CTTGTGCACTTCTGGGGCCAAACAGCGCTGGAGCTGTGCCACCACTATCTGGTGAA 191
Db      1052  CATCTGGATGTTCTGTTCCACATGAAGCCCTGGAGCGGCATCTCCCTGTACATGTTCAA 1111

Qy      192  CCTGATGGTGGCGACCTGCTTTATGTGCTAT---TGCCCTTCTCATCATCACTACTC 248
Db      1112  TTTGGCTCTGGCGACCTTCTTGTAGCTGTGATCTTGGCAGCCCTGATCTTCTACTACTT 1171

Qy      249  ACTAGATGACAGGTGGCCCTTCGGGGAGCTGTCTCTCAAGCTGGTGACATTCCTGTGTTA 308
Db      1172  CAATAAAACAGATGGATCTTCGGGATGCCATGTGTAAACTGCAGAGGTTTCATCTTTCA 1231

Qy      309  TATCAACCTTTACGGCAGCATCTGTCTGACCTGTGATCTCTGTGCAACCACTTCTTAGG 368
Db      1232  TGTGAACCTCTATGGCAGCATCTTGTCTGTGACATGATCAGTGTGCCCAACCGGTACAGCG 1291

Qy      369  TGTGTGCCACCACTGTGTTGCTGCCCTACCGACCCGAGGCATGCTTGGCTGGGCGAC 428
Db      1292  TGTGGTGTACCCCTCAAGTCCCTTGGCGCGCTCAAAAAGAAATGGATCTGTATCAG 1351

Qy      429  CAGCACCACTGGGCCCTGTGTCTCTCAAGCTGTCTGCTGCCACACATGGCCCTTCTCCCA 488
Db      1352  CGTGTGCTGTGGCTCATTTGTGTGGTGGCATCTCCCCCATCTCTTCTACTCAGGTAC 1411

Qy      489  ---GGACTACATCAATGGCCAGATGATCTGGTATGATCATGACCAACAGCAAGATTTGA 545
Db      1412  CGGGGTCCGAAAAACAAACCATCACCTGTTCAGACACCACTTCAGACGAGTACCTGGC 1471

Qy      546  TCGCTTTTTCCTAGCGCATGTTCTGACATTTGTC--TGGCTTTTCTTCCCTCCTTGGT 603
Db      1472  AAGTATTTCATCTACAGCATGTGCAGACCGTGGCCATGTTCTGTGTCCCTTGTGTCT 1531

Qy      604  CATTTGGTGTGTATTTACTGATGTGTCAGAGCTGTGATCAAGCAGAGAGAGAAC 658
Db      1532  GATTTGGGCTGTACGGATTAATTGTGAGAGCTTTGATTTACAAAGATCTGGAC 1586

RESULT 10
US-11-136-527-3178
; Sequence 3178, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3178
; LENGTH: 3288
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-11-136-527-3178

Query Match      10.4%; Score 104.2; DB 11; Length 3288;
Best Local Similarity 51.9%; Pred. No. 9.8e-18;
Matches 309; Conservative 0; Mismatches 278; Indels 8; Gaps 3;

Qy      72  CTACCTCTCCCTGCTACAGTATCATCTTTATCTTAGGGCTGCCACTAAATGGCACTGT 131
Db      775  CTACCTGCTCGGCTCTACATCTTAGTGTTCATCATAGGCTTCCTTGGCAACAGCGTGC 834

Qy      132  CTTGTGCACTTCTGGGGCCAAACAGCGCTGGAGCTGTGCCACCACTATCTGGTGAA 191
Db      835  AATCTGATGTTGTGTTTTCACATGAAGCTTGGAGCGGCATCTCGGTGTACATGTTCAA 894

Qy      192  CCTGATGGTGGCGACCTGCTTTATGTGCTAT---TGCCCTTCTCATCATCACTACTC 248
Db      895  TTTGGCTCTGCGGACCTTTTGTGTGTGCTCACCTACCAGCTCTCATCTTCTACTACTT 954
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Qy 431 GCACCACTGGCCCTGGTGTCTCCAGCTGTGCGCCACACTGGCCTTCTCCACACGG 490  
Db 977 TGGCGGTGGTGTGTGGTGTCTCGTCTCGTCACTTGTCCCATCGTGGTCTTCTCGCGCACGG 918  
Qy 491 ACTACATCAATGGCCAGATGATCTGGTATGATGACATGACGACCAAGAG 537  
Db 917 CGGCCAAGACGACGCGGCTGGCTGCAACATGCTCATGCCCGAG 871

RESULT 13  
US-11-134-811-3  
; Sequence 3, Application US/11134811  
; Publication No. US20060024750A1  
; GENERAL INFORMATION:  
; APPLICANT: Wittamer, Valerie  
; APPLICANT: Communi, David  
; APPLICANT: Vandenbogaerde, Ann  
; APPLICANT: Dethoux, Michel  
; APPLICANT: Parmentier, Marc  
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR  
; FILE REFERENCE: 9409/2043  
; CURRENT APPLICATION NUMBER: US/11/134,811  
; CURRENT FILING DATE: 2005-05-20  
; PRIOR APPLICATION NUMBER: 10/603,566  
; PRIOR FILING DATE: 2003-06-25  
; PRIOR APPLICATION NUMBER: US 60/303,858  
; PRIOR FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: US 09/905,253  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 10/201,187  
; PRIOR FILING DATE: 2001-07-23  
; PRIOR APPLICATION NUMBER: PCT/EP02/07647  
; PRIOR FILING DATE: 2002-07-09  
; NUMBER OF SEQ ID NOS: 94  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1116  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-134-811-3 ;

Query Match 9.4%; Score 94; DB 11; Length 1116;  
Best Local Similarity 50.2%; Pred. No. 3.2e-15;  
Matches 232; Conservative 0; Mismatches 230; Indels 0; Gaps 0;

Qy 70 GTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTAAATGGCACT 129  
Db 115 GTCTTCTGTGGTGTATCTACAGCTTGGTGTCTTCTCGTCTCTAGGCAACGGCTG 174  
Qy 130 GTCTTGTGGCACTTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACCACTATCTGGTG 189  
Db 175 GTGATTGTATCGCCACCTTCAAGATGAAGAAGACCGTGAACACTGTGTGGTTGTCAAC 234  
Qy 190 AACTGATGTGGCGGAGCTGCTTTATGTGTATGCTTATGGCTTCTCATCATCACTACTCA 249  
Db 235 CTGGCTGTGGCGGACTTCTCTTCAACATCTTTTGGCGATGCACATCACTACCGGCC 294  
Qy 250 CTAGATGACAGTGGCCCTTCGGGGAGCTGCTGCAAGCTGGTGCACCTTCTCTTCTAT 309  
Db 295 ATGACTACCACTGGTGTTCGGGAGGCCATGTGAAGATCAGCAACTTCTTCTCAGC 354  
Qy 310 ATCAACCTTTACGGCAGCATCTCTGTGTGACCTGTCATCTCTGTGCCACGATTCCTAGGT 369  
Db 355 CACAACATGTACACGAGCTTCTCTGTGACTGTCACTAGCTTTGACCGCTGCATCTCC 414  
Qy 370 GTGTGCCACCACTGTGTGTGCTGCCCTACCGGACCGCAGGAGTATGCTGTGGGCAAC 429  
Db 415 GTGTGCTCCCGCTGTGTGTCTCCAGAACCCGACAGCATCGGCTGTGGCTATACATGACCTGC 474  
Qy 430 AGCACCACTGGGCGCTGGTGTCTCTCAGCTGTGCCACACTGGCTTCTCCACACG 489  
Db 475 TCGGCGCTGTGGGTCTTGGCTTTCTTTTGTAGCTCCCGGTCCCTGTCTTCCGGGACAC 534

Qy 490 GACTACATCAATGCCAGATGATCTGGTATGACATGACCAAGCAGC 531  
Db 535 GCCAACATTCAATGGGAAGATAACCTGCTTCAACAACTTCAGC 576

RESULT 14  
US-11-136-527-3246  
; Sequence 3246, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3246  
; LENGTH: 1428  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-3246

Query Match 9.2%; Score 92; DB 11; Length 1428;  
Best Local Similarity 56.5%; Pred. No. 1.2e-14;  
Matches 192; Conservative 0; Mismatches 145; Indels 3; Gaps 1;

Qy 50 TCTCAGAAAGTCAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTCTAG 109  
Db 206 TCACCGGGAAGCTGACCCACGCTCTTCTCCCGGTCACTACATCATCTTGTGAATTG 265  
Qy 110 GGCTGCCACTAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGAGCT 169  
Db 266 GTTGGCCAGTAATGGTATGGCCCTCTGGGTCTTCTTCCGAACGAAGAAGCACC 325  
Qy 170 GTGCCACCACTATCTGGTGAACCTGATGTGTGGCCGACCTGCTTTATGTGCTATFGCCCT 229  
Db 326 CTGCTGTGATTTACATGGCCCAACCTGGCCTTGGCAGACCTCTCTCTGTCTATCTGGTTCC 385  
Qy 230 TCTCATCATCACTACTACTCATAGATG---ACAGGTGGCCCTTCGGGGAGGTGCTCTGCA 286  
Db 386 CCCTGAAGATCTCTCAACCTCCATGGCAACGACTGGACCTATGGGGATCGGCTCTGCA 445  
Qy 287 AGCTGGTGCACTTCCCTGTTCTATATCAACCTTTTACGCGCAGCATCTCTGCTGACCTGCA 346  
Db 446 AGGTGCTCATTTGGCTTTTCTACGGCAATATGACTCTCCATCTTTCATGACCTGCC 505  
Qy 347 TCTCTGTGCACCAAGTTCCTAGGTGTGTGCCACCCCACTGTG 386  
Db 506 TCAGCGTGACAGAGTACTGGTGTATCTGTGAACCCCATGGG 545

RESULT 15  
US-11-136-527-2066  
; Sequence 2066, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2066  
; LENGTH: 1423



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; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2066 ;

Query Match      9.0%; Score 90; DB 11; Length 1423;
Best Local Similarity 52.4%; Pred. No. 4.1e-14;
Matches 198; Conservative 0; Mismatches 180; Indels 0; Gaps 0;

Qy 71 TCTACCTCTCCCTGGCTACAGTATCATCTTTATCCTAGGGCTGCCACTAAATGGCACTG 130
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 254 TCGCCATACGCGCCTCTACTCGGCTGTGTGCGCGTGTGGGCTGTGGGCAACGTGCTCG 313
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 131 TCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACCTATCTGGTGA 190
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 314 TCATGTTGGNACTGTCGGGTACACTAAGCTGAAGACGGCCACCACATCTACATCTTCA 373
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 191 ACCTGATGGTGGCCGACCTGCTTTATGTGTATTTGCCCTTCCCTCATCATCACCTACTCAC 250
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 374 ATCTGGCCTTGGCGGATGCGCTGGCCACCAGCACACTGCCCTTCCAGAGCGCCAAGTACC 433
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 251 TAGATGACAGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTCTGTTCTATA 310
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 434 TGATGAAACGTGGCCGTTCGGAGAGCTGTGTGCAAGGCTGTGCTCTCCATTGACTACT 493
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 311 TCAACCTTTACGGCAGCATCCTGCTGCCTGCATCTCTGTGCACAGTTCCTAGGTG 370
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 494 ACAACATGTTACACAGCATCTTCACGCTCACCATGATGAGCGTGGACGGCTACATTGGGG 553
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 371 TGTCCCAACCACTGTGTGCTGCCCTACCGGACCCCGAGGCATGTCCTGGCTGGGCACCA 430
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 554 TCTGCCACCCCTGTCAAGGCTTGGACTTCCGGACACCGGCCAAGGCAAGCTGATCAACA 613
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 431 GCACCACTGGGCCCTGG 448
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 614 TATGCATCTGGGCTTGG 631
Db   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 11:15:22 ; Search time 992 Seconds  
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8352.739 Million cell updates/sec

Title: US-10-088-726-25

Perfect score: 1002

Sequence: 1 atggagaaggggacatgaa.....ggttgaaacagatctgggtaa 1002

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1002	100.0	1002	6	US-10-088-726-25
2	1000.4	99.8	1334	6	US-10-017-161-707
3	1000.4	99.8	1334	6	US-10-292-798-619
4	1000.4	99.8	3143	6	US-10-275-910-1
5	996.4	99.4	1082	6	US-10-023-586B-1
6	996.4	99.4	1082	7	US-10-763-972-1
7	977.4	97.5	1108	7	US-10-072-012-165
8	920.4	91.9	1017	3	US-09-885-453-3
9	920.4	91.9	1017	5	US-10-079-384-5
10	917.2	91.5	1020	6	US-10-023-586B-3
11	917.2	91.5	1020	7	US-10-763-972-3
12	917.2	91.5	1076	7	US-10-333-946-20
13	849.4	84.8	851	6	US-10-275-910-6
14	848.4	84.7	850	6	US-10-275-910-4
15	588	58.7	600	10	US-11-060-756-1747
16	588	58.7	600	10	US-11-060-756-1748
17	588	58.7	600	10	US-11-060-756-6019
18	588	58.7	600	10	US-11-060-756-6020
19	510	50.9	510	3	US-09-782-974C-13
20	510	50.9	510	9	US-10-467-492A-13
21	510	50.9	510	9	US-10-975-979-13
22	510	50.9	510	9	US-10-969-727-13
23	400.4	40.0	681	3	US-09-801-944B-47

Sequence 56, Appl  
Sequence 216, App  
Sequence 722, App  
Sequence 1482, Ap  
Sequence 74, Appl  
Sequence 3861, Ap  
Sequence 431, App  
Sequence 331, App  
Sequence 1, Appli  
Sequence 1068, Ap  
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Sequence 1, Appli  
Sequence 41, Appl  
Sequence 55, Appl  
Sequence 57, Appl  
Sequence 9, Appli  
Sequence 1108, Ap  
Sequence 3796, Ap  
Sequence 222, App  
Sequence 994, App  
Sequence 1071, Ap

#### ALIGNMENTS

##### RESULT 1

US-10-088-726-25

; Sequence 25, Application US/10088726

; Publication No. US20030157558A1

; GENERAL INFORMATION:

; APPLICANT: Matsumoto et al.

; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE-BINDING PROTEIN-COUPLED RECEPTORS A  
; FILE REFERENCE: 62514

; CURRENT APPLICATION NUMBER: US/10/088,726

; CURRENT FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: PCT/JF00/09408

; PRIOR FILING DATE: 2000-12-28

; PRIOR APPLICATION NUMBER: JP 1999-375152

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: JP 2000-101339

; PRIOR FILING DATE: 2000-03-31

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 25

; LENGTH: 1002

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-088-726-25

Query Match 100.0%; Score 1002; DB 6; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 2.6e-303;  
Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGCAAGCTGGGACATGATACATCAGAAACAAGTCTCTGCCAGTCTTCAGAGAAG 60
Db	1	ATGCAAGCTGGGACATGATACATCAGAAACAAGTCTCTGCCAGTCTTCAGAGAAG 60
Qy	61	TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120
Db	61	TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120
Qy	121	AATGGCACTGCTTGTGGCACTTCGGGGCCAAACCAAGCGTGGAGCTGTGCCACACC 180
Db	121	AATGGCACTGCTTGTGGCACTTCGGGGCCAAACCAAGCGTGGAGCTGTGCCACACC 180
Qy	181	TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGCTATTGCCCTTCTCTCATCATC 240
Db	181	TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGCTATTGCCCTTCTCTCATCATC 240
Qy	241	ACCTACTCACTAGATGACAGGTGGGCCCTTCGGGGAGCTGCTCTGCAAGCTGTGCACTTC 300

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Db 241 ACCTACTCCTAGATGAGCTGGCTTGGGAGCTGCTGCAAGCTGGTGCATTC 300
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTCTGTGCACAG 360
Db 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTCTGTGCACAG 360
Qy 361 TTCTAGGTGTGCCACCACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 TTCTAGGTGTGCCACCACTGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Qy 421 CTGGGACCCAGCACCTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 421 CTGGGACCCAGCACCTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Qy 481 TCCACACCGACTACATCAATGGCCAGATGATCTGGTATGACATGACATGACATGACATGACAT 540
Db 481 TCCACACCGACTACATCAATGGCCAGATGATCTGGTATGACATGACATGACATGACATGACAT 540
Qy 541 TTGATCGGCTTTTGGCTAGGGATAGTTCTGACATGTTCTGGCTTTCTTTCCCTCCTT 600
Db 541 TTGATCGGCTTTTGGCTAGGGATAGTTCTGACATGTTCTGGCTTTCTTTCCCTCCTT 600
Qy 601 GGTCAATTTGGTGTGCTATTCACTGATGTCAGGAGCTGATCAAGCCAGAGGAGAACCT 660
Db 601 GGTCAATTTGGTGTGCTATTCACTGATGTCAGGAGCTGATCAAGCCAGAGGAGAACCT 660
Qy 661 CATGAGGACAGGCAACACAGCCGAGCAGCTCATCCGACCATCTACTGCTGCTGG 720
Db 661 CATGAGGACAGGCAACACAGCCGAGCAGCTCATCCGACCATCTACTGCTGCTGG 720
Qy 721 CCTCTTCACTCTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Db 721 CCTCTTCACTCTGTTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 780
Qy 781 CTCTTCTGCTTCTCAGACTGCGAGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
Db 781 CTCTTCTGCTTCTCAGACTGCGAGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 840
Qy 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Qy 901 GGCAAAATAGTCAAGCTCTCCAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Db 901 GGCAAAATAGTCAAGCTCTCCAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
Qy 961 GCTGGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1002
Db 961 GCTGGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1002
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RESULT 2
US-10-017-161-707
; Sequence 707, Application US/10017161
; Publication No. US20030143668A1
; GENERAL INFORMATION:
; APPLICANT: SUWA, MAKIYO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 707
; LENGTH: 1334
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: source
; LOCATION: (1)..(1334)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (201)..(715)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(1134)
US-10-017-161-707

Query Match
Best Local Similarity 99.8%; Score 1000.4; DB 6; Length 1334;
Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGAAGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db 201 ATGGAGAAGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 260
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 261 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 320
Qy 121 AATGGCACTCTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180
Db 321 AATGGCACTCTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 380
Qy 181 TATCTGTGAACCTGATGGTGGCGGACCTGCTCTTTATGTGCTATTGCCCTTCTCATCATC 240
Db 381 TATCTGTGAACCTGATGGTGGCGGACCTGCTCTTTATGTGCTATTGCCCTTCTCATCATC 440
Qy 241 ACCTACTCCTAGATGAGTGGCTTGGGGAGCTGCTCTGCAAGCTGGTGCATTC 300
Db 441 ACCTACTCCTAGATGAGTGGCTTGGGGAGCTGCTCTGCAAGCTGGTGCATTC 500
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTCTGTGCACAG 360
Db 501 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCACTCTCTGTGCACAG 560
Qy 361 TTCTAGGTGTGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 561 TTCTAGGTGTGCCACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
Qy 421 CTGGGACCCAGCACCTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
Db 621 CTGGGACCCAGCACCTGGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 680
Qy 481 TCCACACCGACTACATCAATGGCCAGATGATCTGGTATGACATGACATGACATGACATGACAT 540
Db 681 TCCACACCGACTACATCAATGGCCAGATGATCTGGTATGACATGACATGACATGACATGACAT 740
Qy 541 TTTGATCGGCTTTTGGCTAGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 600
Db 741 TTTGATCGGCTTTTGGCTAGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 800
Qy 601 GGTCAATTTGGTGTGCTATTCACTGATGTCAGGAGCTGATCAAGCCAGAGGAGAACCT 660
Db 801 GGTCAATTTGGTGTGCTATTCACTGATGTCAGGAGCTGATCAAGCCAGAGGAGAACCT 860
Qy 661 CATGAGGACAGGCAACACAGCCGAGCAGCTCATCCGACCATCTACTGCTGCTGG 720
Db 861 CATGAGGACAGGCAACACAGCCGAGCAGCTCATCCGACCATCTACTGCTGCTGG 920
Qy 721 CCTCTTCACTCTGTTTGGTGGCTTCCATATCACTGCTGCTCTTCTACCTCAACATCTG 780
Db 921 CCTCTTCACTCTGTTTGGTGGCTTCCATATCACTGCTGCTCTTCTACCTCAACATCTG 980
Qy 781 CTCTTCTGCTTCTCAGGACTGCGAGCTTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 981 CTCTTCTGCTTCTCAGGACTGCGAGCTTGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1040
Qy 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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Db 1041 GAGGCTCTGGTGTGAGCAGCTGCTCAACCCAGCTCTGTACTTTCTTTCAAGGG 1100  
Qy 901 GCGAARATAGAGTCAGCTCTCCAGAACTGAGGCAAGACAGTTCGGTGGATCCA 960  
Db 1101 GCGAARATAGAGTCAGCTCTCCAGAACTGAGGCAAGACAGTTCGGTGGATCCA 1160  
Qy 961 GCTGGGGAAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1002  
Db 1161 GCTGGGGAAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1202

RESULT 3

US-10-292-798-619  
; Sequence 619, Application US/10292798  
; Publication No. US20030235833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292,798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 619  
; LENGTH: 1334  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; LOCATION: source  
; FEATURE:  
; LOCATION: (1)..(1334)  
; NAME/KEY: CDS  
; LOCATION: (201)..(715)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (834)..(1134)  
US-10-292-798-619

Query Match 99.8%; Score 1000.4; DB 6; Length 1334;  
Best Local Similarity 99.9%; Pred. No. 9.2e-303;  
Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGAGGTGGACATGAATACATCAGGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 60  
Db 201 ATGGAGAGGTGGACATGAATACATCAGGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 260  
Qy 61 TACAAGCAAGTCTACTCTCCCTGGCTACAGTATCATCTTTATCTAGGCTGCCACTA 120  
Db 261 TACAAGCAAGTCTACTCTCCCTGGCTACAGTATCATCTTTATCTAGGCTGCCACTA 320  
Qy 121 AATGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACACC 180  
Db 321 AATGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACACC 380  
Qy 181 TATCTGTGAACCTGATGGTGGCCAGCTCTTTATGTGCTATTGCTCTCTCATCATC 240  
Db 381 TATCTGTGAACCTGATGGTGGCCAGCTCTTTATGTGCTATTGCTCTCTCATCATC 440  
Qy 241 ACCTACTCAGTAGAGAGGTGGCCCTTCGGGGAGCTCTGCAAGCTGGTGCACTTC 300  
Db 441 ACCTACTCAGTAGAGAGGTGGCCCTTCGGGGAGCTCTGCAAGCTGGTGCACTTC 500  
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCTGACCTGATCTCTGTGACCCAG 360  
Db 501 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCTGACCTGATCTCTGTGACCCAG 560

Qy 361 TTCCTAGTGTGTCACCCACTGTGTTGCTTGCCTTACCGACCCGAGGATCCCTCGG 420  
Db 561 TTCCTAGTGTGTCACCCACTGTGTTGCTTGCCTTACCGACCCGAGGATCCCTCGG 520  
Qy 421 CTGGGCACAGCACCACCTGGGCCCTGGTGTCTCTCCAGCTGCTGCCACACTGGCCTTC 480  
Db 621 CTGGGCACAGCACCACCTGGGCCCTGGTGTCTCTCCAGCTGCTGCCACACTGGCCTTC 680  
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGATCATGACACAGCAAGAGAT 540  
Db 681 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGATCATGACACAGCAAGAGAT 740  
Qy 541 TTTGATGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 600  
Db 741 TTTGATGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 800  
Qy 601 GGTCAATTTGGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAACT 660  
Db 801 GGTCAATTTGGTGTGCTATTCACTGATGGTCAGGAGCCTGATCAAGCCAGAGGAGAACT 860  
Qy 861 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGAGCACCCTCTACTGGTGTGG 720  
Db 920 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGAGCACCCTCTACTGGTGTGG 920  
Qy 721 CCTCTTCACTCTGTTTGTGGCCCTTCCATATCACTGGCTCTTCTACCTCACCATCTG 780  
Db 921 CCTCTTCACTCTGTTTGTGGCCCTTCCATATCACTGGCTCTTCTACCTCACCATCTG 980  
Qy 781 CTCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTGAGCCAGCTGTGGCTTCAAGATATG 840  
Db 981 CTCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTGAGCCAGCTGTGGCTTCAAGATATG 1040  
Qy 841 GAGGCTCTGCTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTTCTTTTCAAGGG 900  
Db 1041 GAGGCTCTGCTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTTCTTTTCAAGGG 1100  
Qy 901 GGCAGAAATAGATCAGCTCCTCCAGAACTGAGGCAAGACAGTTCGGTGGAGCATCCA 960  
Db 1101 GGCAGAAATAGATCAGCTCCTCCAGAACTGAGGCAAGACAGTTCGGTGGAGCATCCA 1160  
Qy 961 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1002  
Db 1161 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1202

RESULT 4

US-10-275-910-1  
; Sequence 1, Application US/10275910  
; Publication No. US20030166142A1  
; GENERAL INFORMATION:  
; APPLICANT: Ramakrishnan, Shyam  
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR  
; FILE REFERENCE: 4974.00885  
; CURRENT APPLICATION NUMBER: US/10/275,910  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR APPLICATION NUMBER: US 60/203,582  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/269,857  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 3143  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (520)..(1373)  
US-10-275-910-1

Query Match 99.8%; Score 1000.4; DB 6; Length 3143;  
Best Local Similarity 99.9%; Pred. No. 1.3e-302;

Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGAGAGTGGATGATATACATACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 60  
Db |||||  
Qy 520 ATGAGAGAGTGGATGATATACATACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 579  
Db |||||  
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120  
Db |||||  
Qy 580 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 639  
Db |||||  
Qy 121 AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGTGTGCCACACCC 180  
Db |||||  
Qy 640 AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGTGTGCCACACCC 699  
Db |||||  
Qy 181 TATCTGGTGAACCTGATGTTGGCGCACTGCTTTTATGTGTATTTGTCCTTCTCATCATC 240  
Db |||||  
Qy 700 TATCTGGTGAACCTGATGTTGGCGCACTGCTTTTATGTGTATTTGTCCTTCTCATCATC 759  
Db |||||  
Qy 241 ACCTACTCAGTATGATGACAGTGGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300  
Db |||||  
Qy 760 ACCTACTCAGTATGATGACAGTGGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 819  
Db |||||  
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAAG 360  
Db |||||  
Qy 820 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAAG 879  
Db |||||  
Qy 361 TTCCTAGGTGTGGCAACCACTGTTGTTGGTGGCCCTTACGGGACCGGAGCATGCTCTGG 420  
Db |||||  
Qy 880 TTCCTAGGTGTGGCAACCACTGTTGTTGGTGGCCCTTACGGGACCGGAGCATGCTCTGG 939  
Db |||||  
Qy 421 CTGGGCAACGACCACTGCGGCCCTTGGTGTCTCCAGCTGCTGCCACACTGGCCCTC 480  
Db |||||  
Qy 940 CTGGGCAACGACCACTGCGGCCCTTGGTGTCTCCAGCTGCTGCCACACTGGCCCTC 999  
Db |||||  
Qy 481 TCCCAACGCACTACATCAATGGCCAGATGATCTGCTATGACATGACAGCAAGCAAGAAAT 540  
Db |||||  
Qy 1000 TCCCAACGCACTACATCAATGGCCAGATGATCTGCTATGACATGACAGCAAGCAAGAAAT 1059  
Db |||||  
Qy 541 TTTGATCGGCTTTTGGCTACGGCAATGTTCTGACATTTGTCTGCTTTCTTTCCCTCCTT 600  
Db |||||  
Qy 1060 TTTGATCGGCTTTTGGCTACGGCAATGTTCTGACATTTGTCTGCTTTCTTTCCCTCCTT 1119  
Db |||||  
Qy 601 GGTCAATTTGGTGTCTATTCACATGATGGTCAGAGGCTGATCAAGCCAGAGGAGAACCT 660  
Db |||||  
Qy 1120 GGTCAATTTGGTGTCTATTCACATGATGGTCAGAGGCTGATCAAGCCAGAGGAGAACCT 1179  
Db |||||  
Qy 661 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGAGCACTCTACTGTGTGTGG 720  
Db |||||  
Qy 1180 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGAGCACTCTACTGTGTGTGG 1239  
Db |||||  
Qy 721 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTCTTACCTCACCATCTG 780  
Db |||||  
Qy 1240 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCTCTTACCTCACCATCTG 1299  
Db |||||  
Qy 781 CTCTTCTGCTTCTCAGGACTGCGAGCTTTGATGGGAGCCAGTGTGGCTACAGATATG 840  
Db |||||  
Qy 1300 CTCTTCTGCTTCTCAGGACTGCGAGCTTTGATGGGAGCCAGTGTGGCTACAGATATG 1359  
Db |||||  
Qy 841 GAGGCTCTGTTGATGTGAGCAGCTGCTCAACCCAGTCTCTTCTTTCAAGGGG 900  
Db |||||  
Qy 1360 GAGGCTCTGTTGATGTGAGCAGCTGCTCAACCCAGTCTCTTCTTTCAAGGGG 1419  
Db |||||  
Qy 901 GGCAAAATAGAGTCAAGCTCTCCAGAAACTGAGGAGCAAGAACTGTTGGGTGAGCATCCA 960  
Db |||||  
Qy 1420 GGCAAAATAGAGTCAAGCTCTCCAGAAACTGAGGAGCAAGAACTGTTGGGTGAGCATCCA 1479  
Db |||||  
Qy 961 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1002  
Db |||||  
Qy 1480 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTGGGTAA 1521  
Db |||||

RESULT 5

US-10-023-586B-1

; Sequence 1, Application US/10023586B  
; Publication No. US2003016882A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Ltd. (BP (GB) only)  
; APPLICANT: Pfizer Inc. (US, JP, EP except GB)  
; APPLICANT: Fidock, Mark David  
; TITLE OF INVENTION: No. US2003016882A1el Polypeptide  
; FILE REFERENCE: PC10960AGPR  
; CURRENT APPLICATION NUMBER: US/10/023,586B  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: GB 0030855.1  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/260,563  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: US 60/265,688  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: GB 0101222.8  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1082  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-023-586B-1

Query Match 99.4%; Score 996.4; DB 6; Length 1082;  
Best Local Similarity 99.9%; Pred. No. 1.5e-301;  
Matches 997; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGAGAGAGTGGATGATATACATACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 60  
Db |||||  
Qy 85 ATGAGAGAGTGGATGATATACATACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 144  
Db |||||  
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120  
Db |||||  
Qy 145 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 204  
Db |||||  
Qy 121 AATGGCACTGCTTTGTGGCACTTCTTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 180  
Db |||||  
Qy 205 AATGGCACTGCTTTGTGGCACTTCTTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 264  
Db |||||  
Qy 181 TATCTGTGTGAACCTGATGTTGGCGCACTGCTTTTATGTGTATTTGCTCTTCTCATCATC 240  
Db |||||  
Qy 265 TATCTGTGTGAACCTGATGTTGGCGCACTGCTTTTATGTGTATTTGCTCTTCTCATCATC 324  
Db |||||  
Qy 241 ACCTACTCAGTATGACAGTGGCCCTTTCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300  
Db |||||  
Qy 325 ACCTACTCAGTATGACAGTGGCCCTTTCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 384  
Db |||||  
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAAG 360  
Db |||||  
Qy 385 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAAG 444  
Db |||||  
Qy 361 TTCTTAGTGTGTGGCAACCACTGTTTCCCTACCGCCCTTCCGAGCCCGGAGCATGCTCTGG 420  
Db |||||  
Qy 445 TTCTTAGTGTGTGGCAACCACTGTTTCCCTACCGCCCTTCCGAGCCCGGAGCATGCTCTGG 504  
Db |||||  
Qy 421 CTGGGCAACGAGCAACCACTGCGGCCCTTGGTGTCTTCCAGCTGTCTGCCACACTGGCTTTC 480  
Db |||||  
Qy 505 CTGGGCAACGAGCAACCACTGCGGCCCTTGGTGTCTTCCAGCTGTCTGCCACACTGGCTTTC 564  
Db |||||  
Qy 481 TCCCAACGCACTACATCAATGGCAGATGATCTGTTATGACATGACAGCAAGCAAGAAAT 540  
Db |||||  
Qy 565 TCCCAACGCACTACATCAATGGCAGATGATCTGTTATGACATGACAGCAAGCAAGAAAT 624  
Db |||||  
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGTGTGGCTTTCTTTCCCTCCTT 600  
Db |||||  
Qy 625 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGTGTGGCTTTCTTTCCCTCCTT 684  
Db |||||  
Qy 601 GGTCAATTTGGTGTCTATTCACCTGATGGTTCAGGAGCTGATCAAGCCAGAGGAGAACCT 660  
Db |||||  
Qy 685 GGTCAATTTGGTGTCTATTCACCTGATGGTTCAGGAGCTGATCAAGCCAGAGGAGAACCT 744  
Db |||||

QY 661 CATGAGGACGGCAACACAGCCGAGCCAGGTCCATCCGACCATCTCTACTGCTGTGG 720  
Db CATGAGGACGGCAACACAGCCGAGCCAGGTCCATCCGACCATCTCTACTGCTGTGG 804  
QY 721 CCTCTTCAACCTCTGTTTTGTGCCCCCTTCATATCACTCGCTCTTCTACCTCACCATCTG 780  
Db CCTCTTCAACCTCTGTTTTGTGCCCCCTTCATATCACTCGCTCTTCTACCTCACCATCTG 864  
QY 781 CTTTCTGCTTTCTCAGGACTGCGAGCTCTTATGCGCAGCCAGGTGGCTCACAAGATATG 840  
Db CTTTCTGCTTTCTCAGGACTGCGAGCTCTTATGCGCAGCCAGGTGGCTCACAAGATATG 924  
QY 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTCAAGGGG 900  
Db GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTCAAGGGG 984  
QY 901 GGC AAAAATAGAGTCAGGCTCTCTCAGAAAACCTGAGGCAAGAACTTTGGGTGAGCATCCA 960  
Db GGC AAAAATAGAGTCAGGCTCTCTCAGAAAACCTGAGGCAAGAACTTTGGGTGAGCATCCA 1044  
QY 961 GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGG 998  
Db GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGG 1082

## RESULT 6

US-10-763-972-1  
; Sequence 1, Application US/10763972  
; Publication No. US20040137500A1  
; GENERAL INFORMATION:  
; APPLICANT: PFIZER INC.  
; APPLICANT: Fidock, Mark David  
; TITLE OF INVENTION: Novel Polypeptide  
; FILE REFERENCE: PCI0960B  
; CURRENT APPLICATION NUMBER: US/10/763,972  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: GB 0030855.1  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/260,563  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: US 60/265,688  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: GB 0101222.8  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1082  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-763-972-1

Query Match 99.4%; Score 996.4; DB 7; Length 1082;  
Best Local Similarity 99.9%; Pred. No. 1.5e-301;  
Matches 997; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGGAGAAGGTGGACATGAATACATCAAGGAACTCTGCGAGTTCTCAGAGAAG 60  
Db 85 ATGGAGAAGGTGGACATGAATACATCAAGGAACTCTGCGAGTTCTCAGAGAAG 144  
QY 61 TACAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCCTAGGGCTGCCACTA 120  
Db 145 TACAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCCTAGGGCTGCCACTA 204  
QY 121 AATGSCACTGTCTTGTGGCACTTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 180  
Db 205 AATGSCACTGTCTTGTGGCACTTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 264  
QY 181 TATCTGGTGAACCTGAATGGTGGCCGACCTGCTTTATGTGCTATATGCCCTTCTCATATC 240  
Db 265 TATCTGGTGAACCTGAATGGTGGCCGACCTGCTTTATGTGCTATATGCCCTTCTCATATC 324

QY 241 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGTCTCTCAAGCTGGTGCACATTC 300  
Db ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGTCTCTCAAGCTGGTGCACATTC 384  
QY 301 CTGTTCTATATCAACTTTTACGGCAGCATCTCTGCTGTGACCTGATCTCTGTGACACAG 360  
Db CTGTTCTATATCAACTTTTACGGCAGCATCTCTGCTGTGACCTGATCTCTGTGACACAG 444  
QY 361 TTCTCTAGGTGTGCGCCACCATCTGTGTGCTGCGCTACCGGACCCGAGCATGSCCTGG 420  
Db TTCTCTAGGTGTGCGCCACCATCTGTGTGCTGCGCTACCGGACCCGAGCATGSCCTGG 504  
QY 421 CTGGGCAACGACACCATCTGGGCCCTCTGCTGTCTCTCAGCTGTCTGCCACACTGSCCTTC 480  
Db CTGGGCAACGACACCATCTGGGCCCTCTGCTGTCTCTCAGCTGTCTGCCACACTGSCCTTC 564  
QY 481 TCCACACGGACTACATCAATGGCCAGATGATCTGTGTATGACATGACCCAGCAAGAGAT 540  
Db TCCACACGGACTACATCAATGGCCAGATGATCTGTGTATGACATGACCCAGCAAGAGAT 624  
QY 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTCTGTGCTTTCTTCCCTCCTT 600  
Db TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTCTGTGCTTTCTTCCCTCCTT 684  
QY 601 GGTCAATTTTGGTGTGCTATTCTACCTGATGCTCAGGAGCCTGATCAAGCCAGAGGAGAACT 660  
Db GGTCAATTTTGGTGTGCTATTCTACCTGATGCTCAGGAGCCTGATCAAGCCAGAGGAGAACT 744  
QY 661 CATGAGGACGGCAACACAGCCGAGCAGGTCCATCCGACCATCTCTACTGCTGTGG 720  
Db CATGAGGACGGCAACACAGCCGAGCAGGTCCATCCGACCATCTCTACTGCTGTGG 804  
QY 721 CCTCTTCAACCTCTGTTTTGTGCCCCCTTCCATATCACTCGCTCTTCTACCTCACCATCTG 780  
Db CCTCTTCAACCTCTGTTTTGTGCCCCCTTCCATATCACTCGCTCTTCTACCTCACCATCTG 864  
QY 781 CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGCGCAGCCAGTGTGGCTTCAAGATATG 840  
Db CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGCGCAGCCAGTGTGGCTTCAAGATATG 924  
QY 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCTCAACCCAGTCTCTGTACTTTCTTCAAGGGG 900  
Db GAGGCTCTGCTGAGTGTGAGCAGCTGCTCTCAACCCAGTCTCTGTACTTTCTTCAAGGGG 984  
QY 901 GGC AAAAATAGATCAGGCTCTCTCAGAAAACCTGAGGCAAGAACTTTGGGTGAGCATCCA 960  
Db GGC AAAAATAGATCAGGCTCTCTCAGAAAACCTGAGGCAAGAACTTTGGGTGAGCATCCA 1044  
QY 961 GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGG 998  
Db GCTGGGAGGAAGAGATGCCAGGGTTGAACAGATCTGG 1082

## RESULT 7

US-10-072-012-165  
; Sequence 165, Application US/10072012  
; Publication No. US20040033493A1  
; GENERAL INFORMATION:  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Shinkets, Richard  
; APPLICANT: Li, Li  
; APPLICANT: Gangolli, Esha  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Anderson, David W.  
; APPLICANT: Raestelli, Luca  
; APPLICANT: Miller, Charles E.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Taupier Jr, Raymond J.  
; APPLICANT: Gusev, Vladimir Y.  
; APPLICANT: Colman, Steven D.

```
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 165
; LENGTH: 1108
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-012-165

Query Match      97.5%; Score 977.4; DB 7; Length 1108;
Best Local Similarity 99.7%; Pred. No. 1.4e-295;
Matches 1000; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 ATGAGAGAGGTGGACATGAATACATACAGGAAACAAGGTCTCTGCCAGTTTCTCAGAGAAG 60
Db ATGAGAGAGGTGGACATGAATACATACAGGAAACAAGGTCTCTGCCAGTTTCTCAGAGAAG 155

Qy 61 TACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120
Db TACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 215

Qy 156 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 215
Db TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 275

Qy 121 AATGGCACTGTCTTGTGGCACTCTCTGGGGCAACCAAGCGCTGGAGCTGGCCACCACC 180
Db AATGGCACTGTCTTGTGGCACTCTCTGGGGCAACCAAGCGCTGGAGCTGGCCACCACC 275

Qy 181 TATCTGGTGAACCTGTATGGTGGCCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 240
Db TATCTGGTGAACCTGTATGGTGGCCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 335

Qy 241 ACCTACTACTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db ACCTACTACTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 395

Qy 301 CTGTTCTATATCAACCTTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCCACAG 360
Db CTGTTCTATATCAACCTTTTACGGCAGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 455

Qy 361 TTCTTAGGTGTGCCACCCCACTGTGTGTGCTGCCCTACCGGACCCCGAGCATGCTCTGG 420
Db TTCTTAGGTGTGCCACCCCACTGTGTGTGCTGCCCTACCGGACCCCGAGCATGCTCTGG 515
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RESULT 8
US-09-885-453-3
; Sequence 3, Application US/09885453
; Publication No. US20030088080A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: RECEPTOR GPCR $\alpha$ 10
; FILE REFERENCE: 9409/2082
; CURRENT APPLICATION NUMBER: US/09/885,453
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 09/885,453
; PRIOR FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1017
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DNA sequence
; LOCATION: (1)..(1017)
; OTHER INFORMATION: GPCR $\alpha$ 6 DNA sequence
US-09-885-453-3

Query Match      91.9%; Score 920.4; DB 3; Length 1017;
Best Local Similarity 99.8%; Pred. No. 1e-277;
Matches 932; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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Qy 1 ATGAGAGAGGTGGACATGAATATCATCAGGAAACAAGGTCTCTGCCAGTTTCTCAGAGAAG 60
Db ATGAGAGAGGTGGACATGAATATCATCAGGAAACAAGGTCTCTGCCAGTTTCTCAGAGAAG 144
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Qy 61 TACAAGCAAGTCTACCTCCCTGCGCTACAGTATCATCTTTATCCTAGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCCCTGCGCTACAGTATCATCTTTATCCTAGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAC 180
Db 205 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAC 264
Qy 181 TATCTGGTGAACCTGTATGCTGGCGACCTGTTTATGCTATTGCTTATGCTTCTCTCATATC 240
Db 265 TATCTGGTGAACCTGTATGCTGGCGACCTGTTTATGCTATTGCTTATGCTTCTCTCATATC 324
Qy 241 ACCTACTCATTAGATGACAGGTGGCCCTTCGGGAGCTGCTCTCAAGCTGGTGCACTTC 300
Db 325 ACCTACTCATTAGATGACAGGTGGCCCTTCGGGAGCTGCTCTCAAGCTGGTGCACTTC 384
Qy 301 CTGTTCTATATCAACCTTTAGCGAGCATCTCTGCTGCTGACCTGATCTCTGTGCAACG 360
Db 385 CTGTTCTATATCAACCTTTAGCGAGCATCTCTGCTGCTGACCTGATCTCTGTGCAACG 444
Qy 361 TTCCTAGTGTGTGCCACCACTGTGCTGGCTTACCGGACCCCGAGGCATGCTGG 420
Db 445 TTCCTAGTGTGTGCCACCACTGTGCTGGCTTACCGGACCCCGAGGCATGCTGG 504
Qy 421 CTGGGCAACGACCACTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db 505 CTGGGCAACGACCACTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 564
Qy 481 TCCCAACGAGCACTACATCAATGCGCAGATGATCTGGTATGACATGACAGCAAGAGAT 540
Db 565 TCCCAACGAGCACTACATCAATGCGCAGATGATCTGGTATGACATGACAGCAAGAGAT 624
Qy 541 TTTGATCGGCTTTTGGCTAGCGCATAGTTCTGACATGTTGCTGGCTTTTCCCTCCTT 600
Db 625 TTTGATCGGCTTTTGGCTAGCGCATAGTTCTGACATGTTGCTGGCTTTTCCCTCCTT 683
Qy 601 GGTCAATTTGCTGTGCTATTCATGATGCTCAGGAGCTGATCAAGCCAGAGGAGAACT 660
Db 684 GGTCAATTTGCTGTGCTATTCATGATGCTCAGGAGCTGATCAAGCCAGAGGAGAACT 743
Qy 661 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGGACCACTCTTACTGCTGCTG 720
Db 744 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGGACCACTCTTACTGCTGCTG 803
Qy 721 CCTCTTACCCCTCTGTTTGTGGCTTCCATATCATCTGCTGCTTCTACCTCAACATCTG 780
Db 804 CCTCTTACCCCTCTGTTTGTGGCTTCCATATCATCTGCTGCTTCTTACTCAACATCTG 863
Qy 781 CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCAGTGTGGCTTACAAGATATG 840
Db 864 CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCAGTGTGGCTTACAAGATATG 923
Qy 841 GAGGCCCTCTGCTGAGTGTGAGCAGTCTCAACCCAGTCTCTGATCTTTCTTCAAGGGG 900
Db 924 GAGGCCCTCTGCTGAGTGTGAGCAGTCTCAACCCAGTCTCTGATCTTTCTTCAAGGGG 983
Qy 901 GGCAGCAATAGAGTCAGGCTCTCCAGAACTGA 934
Db 984 GGCAGCAATAGAGTCAGGCTCTCCAGAACTGA 1017
```

RESULT 9  
US-10-079-384-5  
; Sequence 5, Application US/10079384  
; Publication No. US20030108986A1  
; GENERAL INFORMATION:  
; APPLICANT: Communi, Didier  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS COMPRISING G-PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 9409/2132  
; CURRENT APPLICATION NUMBER: US/10/079,384  
; CURRENT FILING DATE: 2002-02-20  
; PRIOR APPLICATION NUMBER: US 09/885,453  
; PRIOR FILING DATE: 2001-06-20

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; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1017  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1017)  
; OTHER INFORMATION:  
US-10-079-384-5
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Query Match 91.9%; Score 920.4; DB 5; Length 1017;  
Best Local Similarity 99.8%; Pred. No. 1e-277;  
Matches 932; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Qy 1 ATGAGAAAGGTGGAGCATGAATACATCACAGGAAACAAAGTCTCTGCCAGTTCTCAGAGAA 60
Db 85 ATGAGAAAGGTGGAGCATGAATACATCACAGGAAACAAAGTCTCTGCCAGTTCTCAGAGAA 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCCTAGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTTATCCTAGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAC 180
Db 205 AATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAC 264
Qy 181 TATCTGTGTAACCTGTATGCTGGCGACCTGCTTTTATGCTATTGCTTATGCTTCTCTCATATC 240
Db 265 TATCTGTGTAACCTGTATGCTGGCGACCTGCTTTTATGCTATTGCTTATGCTTCTCTCATATC 324
Qy 241 ACCTACTCATTAGATGACAGGTGGCCCTTCGGGAGCTGCTCTCAAGCTGGTGCACTTC 300
Db 325 ACCTACTCATTAGATGACAGGTGGCCCTTCGGGAGCTGCTCTCAAGCTGGTGCACTTC 384
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCTGACCTGATCTCTGTGCAACG 360
Db 385 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCTGACCTGATCTCTGTGCAACG 444
Qy 361 TTCCTAGTGTGTGCCACCACTGTGCTGGCTTACCGGACCCCGAGGCATGCTGG 420
Db 445 TTCCTAGTGTGTGCCACCACTGTGCTGGCTTACCGGACCCCGAGGCATGCTGG 504
Qy 421 CTGGGCAACGACCACTGCTGGCCCTTCGGGCTGCTCAGGCTGCTGCCACACTGSCCTTC 480
Db 505 CTGGGCAACGACCACTGCTGGCCCTTCGGGCTGCTCAGGCTGCTGCCACACTGSCCTTC 564
Qy 481 TCCCAACGAGCACTACATCAATGGCCAGATGATCTGGTATGACATGATGACATGACAGAA 540
Db 565 TCCCAACGAGCACTACATCAATGGCCAGATGATCTGGTATGACATGATGACATGACAGAA 624
Qy 541 TTTGATCGGCTTTTGGCTAGCGCATAGTTCTGACATGTTGCTGGCTTTTCCCTCCTT 600
Db 625 TTTGATCGGCTTTTGGCTAGCGCATAGTTCTGACATGTTGCTGGCTTTTCCCTCCTT 683
Qy 601 GGTCAATTTGCTGTGCTATTCATGATGCTCAGGAGCTGATCAAGCCAGAGGAGAACT 660
Db 684 GGTCAATTTGCTGTGCTATTCATGATGCTCAGGAGCTGATCAAGCCAGAGGAGAACT 743
Qy 661 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGGACCACTCTTACTGCTGCTG 720
Db 744 CATGAGGACAGGCAACACAGCCGAGCAGGTCCATCCGGACCACTCTTACTGCTGCTG 803
Qy 721 CCTCTTACCCCTCTGTTTGTGGCTTCCATATCATCTGCTGCTTCTACCTCAACATCTG 780
Db 804 CCTCTTACCCCTCTGTTTGTGGCTTCCATATCATCTGCTGCTTCTTACTCAACATCTG 863
Qy 781 CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCAGTGTGGCTTACAAGATATG 840
Db 864 CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCAGTGTGGCTTACAAGATATG 923
Qy 841 GAGGCCCTCTGCTGAGTGTGAGCAGTCTCAACCCAGTCTCTGATCTTTCTTCAAGGGG 900
Db 924 GAGGCCCTCTGCTGAGTGTGAGCAGTCTCAACCCAGTCTCTGATCTTTCTTCAAGGGG 983
Qy 901 GGCAGCAATAGAGTCAGGCTCTCCAGAACTGA 934
Db 984 GGCAGCAATAGAGTCAGGCTCTCCAGAACTGA 1017
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Db 924 GAGGCCCTCTGTGTAGTGTGACAGCTGCTCAACCCAGTCTCTGTACTTCTTTCAAGGGG 983  
Qy 901 GGCAAAAATAGAGTCAGGCTCCTCCAGAAACTGA 934  
Db 984 GGCAAAAATAGAGTCAGGCTCCTCCAGAAACTGA 1017

RESULT 10  
US-10-023-586B-3  
; Sequence 3, Application US/10023586B  
; Publication No. US20030166882A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Ltd. (EP (GB) only)  
; APPLICANT: Fidoct Inc. (US, JP, EP except GB)  
; APPLICANT: Fidoct, Mark David  
; TITLE OF INVENTION: No. US20030166882A1e1 Polypeptide  
; FILE REFERENCE: PC10960AGR  
; CURRENT APPLICATION NUMBER: US/10/023,586B  
; CURRENT FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: GB 0030855.1  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/260,563  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: US 60/265,688  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: GB 0101222.8  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 1020  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-023-586B-3

Query Match ; 91.5%; Score 917.2; DB 6; Length 1020;  
Best Local Similarity 99.5%; Pred. No. 1.1e-276;  
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 ATGAGAGAGGTGGACATGAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 60  
Db 85 ATGAGAGAGGTGGACATGAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 144

Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120  
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTAGGGCTGCCACTA 204

Qy 121 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180  
Db 205 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 264

Qy 181 TATCTGTGTAACCTGATGTGGCGACCTGCTTTATGTCTATTGCTTATGCCCTTCTCATCATC 240  
Db 265 TATCTGTGTAACCTGATGTGGCGACCTGCTTTATGTCTATTGCTTATGCCCTTCTCATCATC 324

Qy 241 ACCTACTCCTACATGATGACAGTGGCCCTTCGGGAGCTGTCTGCAAGCTGGTGCATTC 300  
Db 325 ACCTACTCCTACATGATGACAGTGGCCCTTCGGGAGCTGTCTGCAAGCTGGTGCATTC 384

Qy 301 CTGTTCTTATATCAACCTTTAGCGGACGATCTGCTGTGCTGACCTGCTCATCTCTGTGCACAG 360  
Db 385 CTGTTCTTATATCAACCTTTAGCGGACGATCTGCTGTGCTGACCTGCTCATCTCTGTGTCACAG 444

Qy 361 TTCTCTAGTGTGTGCCACCACTGTTTGGCTGCGCTACCGGACCGCCGAGCATGCTCTGG 420  
Db 445 TTCTCTAGTGTGTGGCAACCACTGTTTGGCTGCGCTACCGGACCGCCGAGCATGCTCTGG 504

Qy 421 CTGGGCAACGACCACTAGGCGCTCTGGTGTCTCCAGCTGTGCTGCCACACTGGCCCTTC 480  
Db 505 CTGGGCAACGACCACTAGGCGCTCTGGTGTCTCCAGCTGTGCTGCCACACTGGCCCTTC 564

Qy 481 TCCACACGGACTACATCAATGGCCAGTGNATGTGGTATGACATGACCCAGCCAGGAAT 540

Db 565 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACAGCCAGAGAAT 624  
Qy 541 TTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTGTCTGGCTTTCTTTT--CCCTCC 598  
Db 625 TTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTGTCTGGCTTTCTTTTCCCTCC 684

Qy 599 TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAGAGCCTGATCAAGCCAGAGGAGAAC 658  
Db 685 TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAGAGCCTGATCAAGCCAGAGGAGAAC 744

Qy 659 CTGATGAGGACAGCAACACAGCCGAGCCAGGTCCATCCGACCATCTCTACTTGGTGTGT 718  
Db 745 CTGATGAGGACAGCAACACAGCCGAGCCAGGTCCATCCGACCATCTCTACTTGGTGTGT 804

Qy 719 GGCCTCTTCAACCCCTCTGTTTTGTGCCCCCTCCATATCACTCGCTCCTTCTACCTCACCATC 778  
Db 805 GGCCTCTTCAACCCCTCTGTTTTGTGCCCCCTCCATATCACTCGCTCCTTCTACCTCACCATC 864

Qy 779 TGCTTTCTGCTTTCTCAGGACTGCGGAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA 838  
Db 865 TGCTTTCTGCTTTCTCAGGACTGCGGAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA 924

Qy 839 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTTCTTCAAGG 898  
Db 925 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTTCTTCAAGG 984

Qy 899 GGGGCAAAAATAGAGTCAGGCTCCTCCAGAAACTGA 934  
Db 985 GGGGCAAAAATAGAGTCAGGCTCCTCCAGAAACTGA 1020

RESULT 11  
US-10-763-972-3  
; Sequence 3, Application US/10763972  
; Publication No. US20040137500A1  
; GENERAL INFORMATION:  
; APPLICANT: PFIZER INC.  
; APPLICANT: Fidoct, Mark David  
; TITLE OF INVENTION: Novel Polypeptide  
; FILE REFERENCE: PC10960B  
; CURRENT APPLICATION NUMBER: US/10/763,972  
; CURRENT FILING DATE: 2004-01-23  
; PRIOR APPLICATION NUMBER: GB 0030855.1  
; PRIOR FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: US 60/260,563  
; PRIOR FILING DATE: 2001-01-09  
; PRIOR APPLICATION NUMBER: US 60/265,688  
; PRIOR FILING DATE: 2001-02-01  
; PRIOR APPLICATION NUMBER: GB 0101222.8  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 1020  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-763-972-3

Query Match 91.5%; Score 917.2; DB 7; Length 1020;  
Best Local Similarity 99.5%; Pred. No. 1.1e-276;  
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 ATGAGAGAGGTGGACATGAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 60  
Db 85 ATGAGAGAGGTGGACATGAATACATACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 144

Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCCCTA CAGTATCATCTTTATCTAGGGCTGCCACTA 120  
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCCCTA CAGTATCATCTTTATCTAGGGCTGCCACTA 204

Qy 121 AATGGCACTGTCTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180

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Db 205 AATGCACTGTCTTGTGGCACTCTCTGGGGCAAACCAAGCGCTGGAGCTGTGCCACC 264
Qy 181 TATCTGTGAACCTGATGGTGGCGACCTGTTTATGTGCTATTGGCTTATGGCTTCTCATATC 240
Db 265 TATCTGTGAACCTGATGGTGGCGACCTGTTTATGTGCTATTGGCTTATGGCTTCTCATATC 324
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300
Db 325 ACCTACTCACTAGATGACAGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 384
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGCTGATCTCTGTGCAACG 360
Db 385 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGACCTGCTGATCTCTGTGCAACG 444
Qy 361 TTCCTAGTGTGTGCCACCACTGTTGCTGCTGCTTACCGACCCGAGGATGCTGCG 420
Db 445 TTCCTAGTGTGTGGCACCACTGTTGCTGCTGCTTACCGACCCGAGGATGCTGCG 504
Qy 421 CTGGCACGACGACCACTGGGCCCTGGTGGCTCTCCAGCTGCTGCCACACTGGCCTTC 480
Db 505 CTGGCACGACGACCACTGGGCCCTGGTGGCTCTCCAGCTGCTGCCACACTGGCCTTC 564
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAAAT 540
Db 565 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAAAT 624
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCGTTTCTTTT--CCCTCC 598
Db 625 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCGTTTCTTTTCCCTCC 684
Qy 599 TTGCTCATTTTGGTGTGCTATTCTACTGATGTCAGGAGCTGATCAAGCCAGAGAGAAC 658
Db 744 TTGCTCATTTTGGTGTGCTATTCTACTGATGTCAGGAGCTGATCAAGCCAGAGAGAAC 744
Qy 659 CTCTAGAGGACAGGCAACACAGCCCGAGCCAGGTCCTCAACCGAGCTCTTACTGCTGT 718
Db 745 CTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCTCAACCGAGCTCTTACTGCTGT 804
Qy 719 GGCCTCTTCAACCTCTGTTTGTGGCTTTCATATCACTGCTGCTTCTACTCACCATC 778
Db 805 GGCCTCTTCAACCTCTGTTTGTGGCTTTCATATCACTGCTGCTTCTACTCACCATC 864
Qy 779 TGCTTTCTGCTTTCTCAGAGCTGCAGCTCTTGTATGGCAGCAGTGTGGCTTACAAGATA 838
Db 865 TGCTTTCTGCTTTCTCAGAGCTGCAGCTCTTGTATGGCAGCAGTGTGGCTTACAAGATA 924
Qy 839 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGATCTTTTCAAGG 898
Db 925 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGATCTTTTCAAGG 984
Qy 899 GGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 934
Db 985 GGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 1020
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## RESULT 12

US-10-333-946-20

; Sequence 20, Application US/10333946

; Publication No. US20040023252A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; THORNTON, Michael B.

; APPLICANT: ARVIZU, Chandra S.; LAL, Preeti G.

; APPLICANT: BURFORD, Neil; YUE, Henry

; APPLICANT: GANDHI, Aneena R.; ELLIOTT, Vicki S.

; APPLICANT: RAMKUMAR, Javalaxmi; BAUGHN, Mariah R.

; APPLICANT: KALLICK, Deborah A.; CHAWLA, Narinder K.

; APPLICANT: HAFALIA, April J.A.; YAO, Monique G.

; APPLICANT: LU, Yan; TRIBOULEY, Catherine M.

; APPLICANT: POLICKY, Jennifer L.; KEARNEY, Liam

; APPLICANT: GRAUL, Richard C.; WARREN, Bridget A.

; APPLICANT: LEE, Ernestine A.; DING, Li

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: P1-0176 USN

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; CURRENT APPLICATION NUMBER: US/10/333,946
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: PCT/US01/23433
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: US 60/221,478
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/223,268
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/227,054
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 60/231,121
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: US 60/232,243
; PRIOR FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: US 60/232,691
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/235,146
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 1076
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040023252A1 7474806CB1
US-10-333-946-20
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Query Match 91.5%; Score 917.2; DB 7; Length 1076;

Best Local Similarity 99.5%; Pred. No. 1.1e-276;

Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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Qy 1 ATGAGAAGGTGGACATGAATACATCACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 60
Db 141 ATGAGAAGGTGGACATGAATACATCACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 200
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 201 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGGCTGCCACTA 260
Qy 121 AATGGCACTGTCTTGTGGCACTTCTGGGGGCAAAACCAAGCGCTGGAGCTGCCACACC 180
Db 261 AATGGCACTGTCTTGTGGCACTTCTGGGGGCAAAACCAAGCGCTGGAGCTGCCACACC 320
Qy 181 TATCTGTGAACCTGATGTGTGGCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 240
Db 321 TATCTGTGAACCTGATGTGTGGCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 380
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACCTC 300
Db 381 ACCTACTCACTAGATGACAGTGGCCCTTTCGGGGAGCTGCTCTGCAAGCTGGTGCACCTC 440
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCTGACCTGCATCTCTGTGCACGAG 360
Db 441 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTGCTGACCTGCATCTCTGTGCACGAG 500
Qy 361 TTCCTAGTGTGTGCCACCACTGCTGTTGCTGCCCTTACCGGACCCGAGGATGCTCTGG 420
Db 501 TTCCTAGTGTGTGCCACCACTGCTGTTGCTGCCCTTACCGGACCCGAGGATGCTCTGG 560
Qy 421 CTGGGCAACGACCACTGGGGCTGCTGGTGGCTCTCCAGCTGCTGCCACACTGGCCCTTC 480
Db 561 CTGGGCAACGACCACTGGGGCTGCTGGTGGCTCTCCAGCTGCTGCCACACTGGCCCTTC 620
Qy 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAGAAAT 540
Db 621 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACCAAGAGAGAAAT 680
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTTTTCTTTT--CCCTCC 598
Db 681 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATGCTGCTTTTCTTTTCCCTCC 740
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Qy 599 TTGTCATTTTGGTGTCTATTCACTGATGTCAGGAGCCTGATCAAGCCAGAGGAAC 658  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
741 TTGTCATTTTGGTGTCTATTCACTGATGTCAGGAGCCTGATCAAGCCAGAGGAAC 800  
Qy 659 CTCAATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACATCTTACTGGTGT 718  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
801 CTCAATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACATCTTACTGGTGT 860  
Qy 719 GGCCTCTTCAACCTCTCTGTTTGGCCCTTCATATCACTCGCTCTTCTACCTCAACATC 778  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
861 GGCCTCTTCAACCTCTCTGTTTGGCCCTTCATATCACTCGCTCTTCTACCTCAACATC 920  
Qy 779 TGCCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGCGCCAGTGGGCTCAAGATA 838  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
921 TGCCTTCTGCTTCTCAGGACTGCGAGCTCTTGATGCGCCAGTGGGCTCAAGATA 980  
Qy 839 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTTCAAGG 898  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
981 TGGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTTCAAGG 1040  
Qy 899 GGGCAAAATAGAGTCAGGCTCTCCAGAACTGA 934  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1041 GGGCAAAATAGAGTCAGGCTCTCCAGAACTGA 1076

## RESULT 13

US-10-275-910-6  
; Sequence 6, Application US/10275910  
; Publication No. US20030166142A1  
; GENERAL INFORMATION:  
; APPLICANT: Ramakrishnan, Shyam  
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR  
; FILE REFERENCE: 4974.00885  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR FILING DATE: 2002-11-12  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 851  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-275-910-6

Query Match 84.8%; Score 849.4; DB 6; Length 851;  
Best Local Similarity 99.9%; Pred. No. 1.9e-255;  
Matches 850; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAAGGTGGACATGAATACATACAGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 61 TACAGGAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTATCTAGGCTGCCACTA 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 61 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTATCTAGGCTGCCACTA 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 121 AATGGCACTGCTTGTGGCACTCTCTGGGCGCAACCAAGCGCTGGAGCTGGCCACCACC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 121 AATGGCACTGCTTGTGGCACTCTCTGGGCGCAACCAAGCGCTGGAGCTGGCCACCACC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 181 TATCTGTGAACCTGATGTTGGCCGACCTGTTTATGTGCTATTGCTTCTCCCTCATCATC 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 181 TATCTGTGAACCTGATGTTGGCCGACCTGTTTATGTGCTATTGCTTCTCCCTCATCATC 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTGGGAGCTGCTCTGCAAGCTGGTGCATTC 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 241 ACCTACTCACTAGATGACAGTGGCCCTTGGGAGCTGCTCTGCAAGCTGGTGCATTC 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 301 CTGTTCTATATCAACCTTTTACGGGAGCATCTGCTGCTGACCTCATCTCTGTGCACCAG 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 301 CTGTTCTATATCAACCTTTTACGGCAGCATCTCTGCTGACCTGCACTCTCTGTGCACCAG 360  
Qy 361 TTCTTAGTGTGTGGCCACCACTGTGTGTGCTGCCCTACCGGACCGCAGGCATGCTCTGG 420  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
361 TTCTTAGTGTGTGGCCACCACTGTGTGTGCTGCCCTACCGGACCGCAGGCATGCTCTGG 420  
Qy 421 CTGGGCAACAGCAGCAACCTCTGGGCCCTCTCCAGCTGCTGCCACACACTGGCCCTTC 480  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
421 CTGGGCAACAGCAGCAACCTCTGGGCCCTCTCCAGCTGCTGCCACACACTGGCCCTTC 480  
Qy 481 TCCACACGAGCTACATCAATGCGCCAGATGATCTGGTATGACATGACACGAGCAAGAAAT 540  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
481 TCCACACGAGCTACATCAATGCGCCAGATGATCTGGTATGACATGACACGAGCAAGAAAT 540  
Qy 541 TTTGATCGGCTTTTGGCTTAGGCAATGTTCTGACATGTTCTGGCTTTCTTTCCCTCTT 600  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
541 TTTGATCGGCTTTTGGCTTAGGCAATGTTCTGACATGTTCTGGCTTTCTTTCCCTCTT 600  
Qy 601 GGTCAATTTGGTGTCTATTCACTGATGTCAGAGCTGATCAAGCCAGAGGAACCT 660  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
601 GGTCAATTTGGTGTCTATTCACTGATGTCAGAGCTGATCAAGCCAGAGGAACCT 660  
Qy 661 CATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCACTCTACTGTGTGG 720  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
661 CATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGAGCACTCTACTGTGTGG 720  
Qy 721 CTTCTTCAACCTCTGTTTGTGCTTCCATATCACTGCTCTTCTTACCTCACCATCTG 780  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
721 CTTCTTCAACCTCTGTTTGTGCTTCCATATCACTGCTCTTCTTACCTCACCATCTG 780  
Qy 781 CTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGGCAGCCAGTGTGGCCCTACAAGATATG 840  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
781 CTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGGCAGCCAGTGTGGCCCTACAAGATATG 840  
Qy 841 GAGGCTCTGG 851  
Db |||||||||||  
841 GAGGCTCTGG 851

## RESULT 14

US-10-275-910-4  
; Sequence 4, Application US/10275910  
; Publication No. US20030166142A1  
; GENERAL INFORMATION:  
; APPLICANT: Ramakrishnan, Shyam  
; TITLE OF INVENTION: REGULATION OF HUMAN P2Y-LIKE G PROTEIN-COUPLED RECEPTOR  
; FILE REFERENCE: 4974.00885  
; CURRENT FILING DATE: 2002-11-12  
; PRIOR FILING DATE: 2002-11-12  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR FILING DATE: 2001-02-21  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 850  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-275-910-4

Query Match 84.7%; Score 848.4; DB 6; Length 850;  
Best Local Similarity 99.9%; Pred. No. 3.8e-255;  
Matches 849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAAGGTGGACATGAATACATACAGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 ATGGAAGGTGGACATGAATACATACAGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 60  
Qy 61 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTATCTAGGCTGCCACTA 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 TACAAGCAAGTCTACCTCTCCCTGCGCTACAGTATCATCTTATCTAGGCTGCCACTA 120

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Qy 121 AATGGCACTGTCTGTGGCACTTCTGGGGCAAACCAAGCGCTGGAGCTGTGCCACCAAC 180
Db 121 AATGGCACTGTCTGTGGCACTTCTGGGGCAAACCAAGCGCTGGAGCTGTGCCACCAAC 180
Qy 181 TATCTGTGAACCTGATGTGGCGAAGCTGCTTTATGTGCTATTTGCGCTTCTCATCATC 240
Db 181 TATCTGTGAACCTGATGTGGCGAAGCTGCTTTATGTGCTATTTGCGCTTCTCATCATC 240
Qy 241 ACCTACTACATAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTCAAGCTGGTGCATTC 300
Db 241 ACCTACTACATAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTCAAGCTGGTGCATTC 300
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGCAATCTCTGTGCAACAG 360
Db 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGCAATCTCTGTGCAACAG 360
Qy 361 TTCTAGGTGTGGCCACCACTGTGTTGCTGTGCTTACCGGACCGGAGGCAATGCTGCTGG 420
Db 361 TTCTAGGTGTGGCCACCACTGTGTTGCTGTGCTTACCGGACCGGAGGCAATGCTGCTGG 420
Qy 421 CTGGGCAACGACCACTGTGGGCGCTGTGGTGTCTCCAGCTGCTGCCACACTGGCCTTC 480
Db 421 CTGGGCAACGACCACTGTGGGCGCTGTGGTGTCTCCAGCTGCTGCCACACTGGCCTTC 480
Qy 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGCTATGATGACATGACAGCCAAAGAAAT 540
Db 481 TCCACACGAGCTACATCAATGGCCAGATGATCTGCTATGATGACATGACAGCCAAAGAAAT 540
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTCTTTTCCCTCCTT 600
Db 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTCTTTTCCCTCCTT 600
Qy 601 GGTCAATTTGGTGTGCTATTCACTGATGGTCAGAGGCTGATCAAGCCAGAGGAACCT 660
Db 601 GGTCAATTTGGTGTGCTATTCACTGATGGTCAGAGGCTGATCAAGCCAGAGGAACCT 660
Qy 661 CATGAGACAGGCAACACAGCCGAGCGAGTGCATCCGAGACCATCTCTGCTGTGG 720
Db 661 CATGAGACAGGCAACACAGCCGAGCGAGTGCATCCGAGACCATCTCTGCTGTGG 720
Qy 721 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATPATCATCTGCTTCTTACCTTCAACATCTG 780
Db 721 CCTCTTCAACCTCTGTTTGTGGCCCTTCCATPATCATCTGCTTCTTACCTTCAACATCTG 780
Qy 781 CTTTCTGCTTCTCAGAGCTGCCAGCTTTCATGTCAGCAGCAGTGTGGCTTCAAGATATG 840
Db 781 CTTTCTGCTTCTCAGAGCTGCCAGCTTTCATGTCAGCAGCAGTGTGGCTTCAAGATATG 840
Qy 841 GAGGCTCTG 850
Db 841 GAGGCTCTG 850
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## RESULT 15

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US-11-060-756-1747
; Sequence 1747, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1747
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-1747
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Query Match 58.7%; Score 588; DB 10; Length 600;
Best Local Similarity 99.8%; Pred. No. 1.7e-173;
Matches 599; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 336 GCTGACCTGCAATCTCTGTGCAACAGTTTCTAGTGTGTGCCACCACTGTGTTTCTGCTGCC 395
Db 1 GCTGACCTGCAATCTCTGTGCAACAGTTTCTAGTGTGTGCCACCACTGTGTTTCTGCTGCC 60
Qy 396 CTACCGGACCGGAGGCAATGCTTGGCTGGGACAGACCACTTGGGCGCTTGGTGGTCT 455
Db 61 CTACCGGACCGGAGGCAATGCTTGGCTGGGACAGACCACTTGGGCGCTTGGTGGTCT 120
Qy 456 CCAGCTCTGCTGCCACACTGGGCTTCTCCACACAGGACTTACATCAATGAGCCAGATGATCTG 515
Db 121 CCAGCTCTGCTGCCACACTGGGCTTCTCCACACAGGACTTACATCAATGAGCCAGATGATCTG 180
Qy 516 GTATGACATGACACAGCCAGAGAAATTTGATCGGCTTTTGGCTTACGGCATAAGTTCTGAC 575
Db 181 GTATGACATGACACAGCCAGAGAAATTTGATCGGCTTTTGGCTTACGGCATAAGTTCTGAC 240
Qy 576 ATTGTCTGGCTTTTCTTCCCTCTTGGTGTCTTTTGGTGTCTATTCTACTGATGTCAGGA 635
Db 241 ATTGTCTGGCTTTTCTTCCCTCTTGGTGTCTTTTGGTGTCTATTCTACTGATGTCAGGA 300
Qy 636 GCCTGATCAAGCCAGAGAGGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCA 695
Db 301 GCCTGATCAAGCCAGAGAGGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTCCA 360
Qy 696 TCCGGACCATCTACTGCTGTGGCTCTTTCACCTCTGTTTGTGGCCCTTCCATATCA 755
Db 361 TCCGGACCATCTACTGCTGTGGCTCTTTCACCTCTGTTTGTGGCCCTTCCATATCA 420
Qy 756 CTGCTCTCTTCTACCTCAACATCTGCTTCTGCTTCTCAGGACTGCGCAGCTCTTGATGG 815
Db 421 CTGCTCTCTTCTACCTCAACATCTGCTTCTGCTTCTCAGGACTGCGCAGCTCTTGATGG 480
Qy 816 CAG-CCAGTGTGGCTTCAAGATATGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAAC 874
Db 481 CAGCCAGTGTGGCTTCAAGATATGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAAC 540
Qy 875 CCAGTCTCTGATCTTCTTCAAGGGGGCAAAAAATAGAGTCAGGCTCTCTCCAGAACTGA 934
Db 541 CCAGTCTCTGATCTTCTTCAAGGGGGCAAAAAATAGAGTCAGGCTCTCTCCAGAACTGA 600
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 10:35:46 ; Search time 5415 Seconds  
(without alignments)  
10518.400 Million cell updates/sec

Title: US-10-088-726-25

Perfect score: 1002  
Sequence: 1 atggagaaggcgacatgaa.....ggttgacacagatctgggtaa 1002

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: gb.ba.\*

2: gb.in.\*

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4: gb.om.\*

5: gb.ov.\*

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8: gb.pr.\*

9: gb.ro.\*

10: gb.scs.\*

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12: gb.un.\*

13: gb.vi.\*

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15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	1002	100.0	1002	6	BD095704 Novel gua
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3	1000.4	99.8	1334	6	AX646427 Sequence
4	1000.4	99.8	1334	8	AB065670 Homo sapi
5	1000.4	99.8	3143	6	AX365511 Sequence
6	1000.4	99.8	164502	14	AC026960 Homo sapi
7	1000.4	99.8	167084	8	AC092999 Homo sapi
8	996.4	99.4	1082	6	BD187416 Novel pol
9	996.4	99.4	1082	6	AX458306 Sequence
10	989.4	98.7	163958	14	AC021773 Homo sapi
11	977.4	97.5	1108	6	AX921825 Sequence
12	921.4	92.0	1019	8	AF411108 Homo sapi
13	917.2	91.5	1020	6	BD187417 Novel pol
14	917.2	91.5	1020	6	AX458308 Sequence
15	917.2	91.5	1076	6	AX375230 Sequence
16	848.4	84.7	850	6	AX365514 Sequence
17	717.8	71.6	1140	6	CQ734310 Sequence
18	635.8	63.5	184377	9	AC121579 Mus muscu

c	19	635.8	63.5	192485	9	AC135635	AC135635 Mus muscu
	20	627.2	62.6	250610	14	AC120742	AC120742 Rattus no
	21	627.2	62.6	276127	14	AC116265	AC116265 Rattus no
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	23	510	50.9	510	6	AX521817	AX521817 Sequence
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	25	374	37.3	585	6	AX244727	AX244727 Sequence
	26	237.4	23.7	1163	5	GP22V3	X98283 G domestica
	27	229.4	22.9	1074	5	AF069555	AF069555 Melagris
	28	229.4	22.9	2025	6	AR270919	AR270919 Sequence
	29	229.4	22.9	2025	6	AR559307	AR559307 Sequence
	30	229.4	22.9	2025	6	AX548931	AX548931 Sequence
	31	229.4	22.9	2025	8	HSU07225	U07225 Homo sapien
	32	227.8	22.7	1417	4	AY620400	AY620400 Sus scrofa
	33	227.8	22.7	2257	8	BC028135	BC028135 Homo sapi
	34	226.2	22.6	1134	8	AY136753	AY136753 Homo sapi
	35	226.2	22.6	1974	6	CQ720945	CQ720945 Sequence
	36	226.2	22.6	2681	8	BC012104	BC012104 Homo sapi
	37	226.2	22.6	123185	14	AP000587	AP000587 Homo sapi
	38	226.2	22.6	196988	8	AP002761	AP002761 Homo sapi
	39	221.4	22.1	240239	14	AC152268	AC152268 Bos taurus
	40	205.4	20.5	1842	6	I34573	I34573 Sequence 1
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## ALIGNMENTS

### RESULT 1

BD095704

LOCUS

DEFINITION

BD095704

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD095704 1002 bp DNA linear PAT 27-AUG-2002  
Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use.  
BD095704  
BD095704.1 GI:22641292  
WO 0148188-A/16.  
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Matsumoto, S., Oda, T., Saito, Y., Noriyuki, Morikawa, Yoshida, K., Suwa, M., Sugiyama, T., Kishimoto, T., Kanzaki, K., Yasuda, S. and Inoue, Y.  
Novel guanosine triphosphate-bound protein-coupled receptors and genes encoding them, and their production and use  
Patent: WO 0148188-A 16 05-JUL-2001;  
HELIIX RESEARCH INSTITUTE, SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI MORIKAWA, KENJI YOSHIDA, MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI, SHINICHIRO YASUDA, YOSHIHISA INOUE  
OS Homo sapiens (human)  
PN WO 0148188-A/16  
PD 05-JUL-2001  
PR 28-DEC-1999 JP 99P 375152, 31-MAR-2000 JP 00P 101339 PI  
SHUNICHIRO MATSUMOTO, TAMAKI ODA, YOKO SAITO, NORIYUKI PI  
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PI MAKIKO SUWA, TOMOYASU SUGIYAMA, TOSHIMITSU KISHIMOTO, KOJI KANZAKI,  
SHINICHIRO YASUDA, YOSHIHISA INOUE  
PC C12N1/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C07K14/705, PC  
C07K16/28  
PC C12P21/02, C12Q1/02, C12Q1/68, A61K31/711, A61K48/00, A61P43/00, PC  
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	Hominidae; Homo.
REFERENCE	1
AUTHORS	Suwa, M., Asai, K., Akiyama, Y. and Aburatani, H.
TITLE	Guanosine triphosphate-binding protein coupled receptors



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DEFINITION Sequence 1 from Patent WO0185764.
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VERSION AX365511.1 GI:18873666
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Hominidae; Homo.
REFERENCE 1
AUTHORS Ramakrishnan,S.
TITLE Regulation of human p2y-like g protein-coupled receptor
JOURNAL Patent: WO 0185764-A 1 15-NOV-2001;
Bayer Aktiengesellschaft (DE)
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AC026960
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Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 164502)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
TITLE Homo sapiens chromosome 3, clone RP11-170K4
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 164502)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Boguslavskiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
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Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (25-MAR-2000) Whitehead Institute/MIT Center for Genome
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COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 13, 2000 this sequence version replaced g1:7328839.  
All repeats were identified using RepeatMasker:  
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http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
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Center clone name: 170\_K\_4  
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Chemistry: Dye-terminator Big Dye; 100% of reads  
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\* NOTE: This is a 'working draft' sequence. It currently  
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\* is not known and their order in this sequence record is  
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\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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Qy	361	TTCTAGTGTGTGCCACCACTGTGTTGCTGCCCTACCGAACCGCAGGACATGCCCTGG	420
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Qy	661	CATGAGGACGGCAACACAGCCGACGAGTCCATCCGGACCACTCTACTGTTGTGTGG	720
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VERSION	AC092999.3	GI:19033407	
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Hominiidae; Homo.			
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Direct Submission			
Unpublished			
2 (bases 1 to 167084)			
Worley,K.C.			
Direct Submission			
Submitted (09-AUG-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
3 (bases 1 to 167084)			
Worley,K.C.			
Direct Submission			
Submitted (01-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
4 (bases 1 to 167084)			
Worley,K.C.			
Direct Submission			
Submitted (29-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
5 (bases 1 to 167084)			
Worley,K.C.			
Direct Submission			
Submitted (30-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA			
On Mar 1, 2002 this sequence version replaced gi:18139250.			
INFORMATION: <a href="http://www.hgsc.bcm.tmc.edu/">http://www.hgsc.bcm.tmc.edu/</a> or email <a href="mailto:gc-help@bcm.tmc.edu">gc-help@bcm.tmc.edu</a>			
<hr/>			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
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TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

#### ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

#### QUALSTAT-REPORT.

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RESULT 11
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
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Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Hominidae; Homo.
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JOURNAL
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Curagen Corporation (US)
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VERSION AF411108.1 GI:16566321
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SOURCE Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
Discovery and mapping of ten novel G protein-coupled receptor genes
Gene 275 (1), 83-91 (2001)
JOURNAL 11574155
PUBMED
REFERENCE 2 (bases 1 to 1019)
Lee,D.K., Nguyen,T., Lynch,K.R., Cheng,R., Vanti,W.B., Arkhitko,O.,
Lewis,T., Evans,J.F., George,S.R. and O'Dowd,B.F.
Direct Submission
JOURNAL Submitted (17-AUG-2001) Department of Pharmacology, University of
Toronto, 8 Taddle Creek Rd. Rm. 4353, Toronto, Ont M5S 1A8, Canada
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Qy 840 GGAGGCTCTGGTGAAGTGTGAGCAGCTGCCCTCAACCCAGTCCCTCTCTACTCTTCTTCAAGGG 899
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DEFINITION BD187417
ACCESSION BD187417
VERSION BD187417.1 GI:32997156
KEYWORDS JP 2003009885-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homidae; Homo.
REFERENCE 1 (bases 1 to 1020)
Fidock,M.D.
AUTHORS Novel polypeptide
TITLE Patent: JP 2003009885-A 2 14-JAN-2003;
JOURNAL Pfizer Ltd (EP(GB) only), Pfizer Inc (US JP EP except GB)
COMMENT OS Homo sapiens
PN JP 2003009885-A/2
PD 14-JAN-2003
PF 17-DEC-2001 JP 2001382707
PR 18-DEC-2000 GB 0030855.1,17-JAN-2001 GB 0101222.8 PI
mark david fidock
CC

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Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

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RESULT 15  
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LOCUS AX375230 1076 bp DNA linear PAT 01-MAR-2002  
DEFINITION Sequence 20 from Patent WO0210387.  
ACCESSION AX375230  
VERSION AX375230.1 GI:19169948  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE 1  
AUTHORS Thornton, M., Patterson, C., Lal, P., Burford, N., Yue, H., Gandhi, A. R.,  
Elliot, V. S., Runkumar, J., Baughn, M. R., Kallick, D. A., Walla, N. K.,  
Hafalia, A. J., Yao, M. G., Lu, Y., Tribouley, C. M., Policky, J. L.,  
Kearney, L., Graul, R. C., Warren, B. A. and Ding, L.  
G-Protein coupled receptors  
Patent: WO 0210387-A 20 07-FEB-2002;  
Incyte Genomics, Inc. (US)

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ORIGIN

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Best Local Similarity 99.5%; Pred. No. 2.1e-218;  
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
9840.508 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	226.2	22.6	1138	11 DQ052983	DQ052983 Homo sapi
2	202.2	20.2	2542	4 AK017378	AK017378 Mus muscu
3	202.2	20.2	3001	4 AK005013	AK005013 Mus muscu
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5	179.2	17.9	693	6 CD217676	CD217676 pgrin.pk0
6	177.2	17.7	1073	11 DQ052984	DQ052984 Pan trogl
7	164.8	16.4	987	10 AY400797	AY400797 Homo sapi
8	164.8	16.4	1425	4 CR624871	CR624871 full-length
9	164.8	16.4	1515	4 CR612681	CR612681 full-length
10	164.8	16.4	1532	4 CR618945	CR618945 full-length
11	164.8	16.4	1564	4 CR626266	CR626266 full-length
12	164.8	16.4	1589	4 CR626754	CR626754 full-length
13	164.8	16.4	1592	4 CR605588	CR605588 full-length
14	164.8	16.4	1594	4 CR606834	CR606834 full-length
15	164.8	16.4	1638	4 CR617080	CR617080 full-length
16	164.8	16.4	1651	4 CR597500	CR597500 full-length
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18	164.8	16.4	1890	4 CR598765	CR598765 full-length
19	163.4	16.3	925	5 BX704227	BX704227 BX704227
20	163.2	16.3	1577	4 CR860841	CR860841 Pongo pyg
21	160.4	16.0	4439	4 AK076364	AK076364 Mus muscu
22	157.2	15.7	810	8 CX444959	CX444959 JGI_XZG10

23	157.2	15.7	987	10 AY400798	AY400798 Pan trogl
24	155.6	15.5	840	8 CX5113496	CX5113496 JGI_XZG57
25	155.4	15.5	802	8 DN025359	DN025359 JGI_CAARS
26	154.8	15.4	639	7 CV028613	CV028613 7176 Full
27	154.8	15.4	643	7 CV030363	CV030363 9460 Full
28	150.4	15.0	987	10 AY400799	AY400799 Mus muscu
29	145.2	14.5	639	6 CA352828	CA352828 624212 NC
30	142.8	14.3	641	5 BQ396255	BQ396255 NISC ng19
31	141.8	14.2	627	1 AL675845	AL675845 AL675845
32	141.2	14.1	1090	5 BX397648	BX397648 BX397648
33	140.6	14.0	846	7 CV114223	CV114223 AGENCOURT
34	140.2	14.0	1168	1 AL561864	AL561864 AL561864
35	140	14.0	1023	5 BX332649	BX332649 BX332649
36	138.4	13.8	775	8 DR006403	DR006403 TC109532
37	136.4	13.6	1815	7 CN210812	CN210812 RJA041C08
38	135.2	13.5	1013	4 CR614658	CR614658 full-length
39	133.2	13.3	470	7 CO959779	CO959779 AGENCOURT
40	131	13.1	1057	5 BX381744	BX381744 BX381744
41	130	13.0	1090	4 CR598708	CR598708 full-length
42	129.8	13.0	899	5 BQ959110	BQ959110 AGENCOURT
43	127.6	12.7	1035	5 BX379990	BX379990 BX379990
44	127.4	12.7	1042	5 BX397649	BX397649 BX397649
45	127.2	12.7	1095	5 BX358251	BX358251 BX358251

#### ALIGNMENTS

RESULT 1	DQ052983	Homo sapiens P2RY2 gene, VIRTUAL TRANSCRIPT, partial sequence,	1138 bp	DNA linear	GSS 02-JUN-2005
LOCUS	DQ052983	g genomic survey sequence.			
ACCESSION	DQ052983				
VERSION	DQ052983.1	GI:56898930			
KEYWORDS	GSS.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1138)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees				
JOURNAL	(er) PLOS Biol. 3 (6), E170 (2005)				
PUBMED	15869325				
REFERENCE	2 (bases 1 to 1138)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				
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Best Local Similarity	56.3%	Pred. No. 6e-50;			
Matches 485;	Conservative 0;	Mismatches 368;	Indels 8;	Gaps 3;	





with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B

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DB 616 GTGCTCGGGTGTGCTGAACGCTGCTCTATATCTTCTATGCGCGCTCAAAACC 675  
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DB 676 TGGACGCTCCACCACTACATGTTTACCTGGCAGTTTTCGGATCTCTCTACCGAGG 735  
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DB 736 TCCCTGCCGCTGTTGTTTATTACTACGCCCGGGGTGACCACTGGCCATTAGCACGGTG 795  
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DB 796 CTCTGCAAGCTGGTGGTGTCTCTTCTACACCACTCTACTGCGAGCATCTCTTCTCCTC 855  
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QY 460 CTGCTGCCACAGTGGCTTCTCCACACGGAATACATCAATGGCCAGATGATCTGGTAT 519  
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DB 1276 CGCACCTCTACTACTCTCTCCGAT--CACTTGACCTCTAGCTGCCACACCTCAACGCC 1332  
QY 818 GCCAGTGGGCTCAAGATATGAGGCTCTGGTGTGAGTGTGAGCAGCTGCTCAACCCA 877  
DB 1333 ATCAACATGGCATATAGATCAACCGCGCTGGCCAGGCAACAGTGTGTGTGACCGG 1392  
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AK005013  
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ACCESSION AK005013  
VERSION AK005013.2 GI:26339698  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sun, I., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexed capillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11076861  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
PUBMED 11076861  
REFERENCE 6  
AUTHORS Group Phase I to 3001)

**AUTHORS** Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ono, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

**TITLE** Direct Submission

**JOURNAL** Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

**COMMENT** On Dec 10, 2002 this sequence version replaced gi:12836638. Please visit our web site (<http://genome.gsc.riken.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCGCAACGCGAGTTTCTTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGAGATCGACGATCAATTAATTAATTAACCCGCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: XhoI.

**FEATURES** Location/Qualifiers

1..3001

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="PANTOM.DB:1300015C04"

/db\_xref="taxon:10090"

/clone="1300015C04"

/sex="male"

/tissue type="liver"

/clone lib="RIKEN full-length enriched mouse cDNA library"

/dev stage="adult"

477..1598

/note="unnamed protein product; PURINERGIC RECEPTOR P2Y, G-PROTEIN COUPLED 2 (SPTR|09CE24, evidence: FASTY, 100%ID, 100%length, match=1119)

putative"

/codon\_start=1

/protein\_id="BAB23746.1"

/db\_xref="GI:12836639"

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2982..2987

/note="putative"

3001

/note="putative"

**polyA\_signal**

**polyA\_site**

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 Best Local Similarity 54.6%; Pred. No. 2.6e-43;  
 Matches 470; Conservative 0; Mismatches 383; Indels 8; Gaps 3;  
 43 TGCAGTTCTCAGAGAAGTACAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTT 102

Db 549 TGTGCTTCAACGAGGACTTCAAGTAGCTGCTGTTGCCCGTGTCTATGCGGTGGTGTGC 608

Qy 103 ATCTTAGGGCTGGCACCATAAATGACACTGTCTTGTGGCAGCTTCTGGGGCCAAACCAAGCGC 162

Db 609 GTGCTCGGGTTGTGGCTGGAAGCTCGTGGCTCTCTATATCTTCTATGCGCGCTCAAAACC 668

Qy 163 TGGAGCTGTGCCACCACTATCTATCTGTGGTGAACCTGATGTTGGCCGACCTGCTTTATGTGCTA 222

Db 669 TGGAAACGCTCCACCACTACATGTTTCACTCGGCAGTTCGGAGCTCTCTCTACGCGAGCG 728

Qy 223 T---TGCCCTTCTCATCATCACTCACTACTAGATGACAGGTGGCCCTTTCGGGGAGCTG 279

Db 729 TCCCTGCGCGTGTGGTTTATTACTAGCCCGGGGTGACCACTGGCCATTTAGCACGGTG 788

Qy 280 CTCTGCAAGCTGTGCACTTCTCTCTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCTG 339

Db 789 CTCTGCAAGCTGTGGGTTTCTCTTCTACACCAACCTCTACTGCGAGCATCTCTTCTCTC 848

Qy 340 ACCTGATCTCTGTGCAACCAAGTTCTTAGGTGTGTGCCACCACTGTGTTGCTGCGCCCTAC 399

Db 849 ACCTGATCAGCGTGCACCGGTGCTGGGAGTCTCTGCGCCTCTGCACTCCCTGCGGTGG 908

Qy 400 CGGACCGCGAGGATGCTGCTGGCTGGGCACACGACCACTGGGCCCTGGTGGTCTCTCCAG 459

Db 909 GGGCGGGCGCGTTATGCGCGCGGGGTGGTGGCGGTGTGTGGGTGTGGTGGTGGTGGTGG 968

Qy 460 CTGCTGCCACACACTGGCGCTTCTCCACACGGAATACATCAATGGCCAGATGATCTGGTAT 519

Db 969 CAGGCACCGTGTCTACTTCTGTCACCAACAGGCTGGGGGAACCGGATCACTTGGCAT 1028

Qy 520 GATGACACGACCAAGAGAAATTTGATCGGCTTTTGGCTTACGGCATAGTTCTG--ACAT 577

Db 1029 GACACCTCGGCCCGAGAGCTCTTTAGCCATTTTGTGGCTTTACAGCTCCGTCATGCTGGGT 1088

Qy 578 TGTCTGGCTTCTTCTCCCTCTTGTGTCATTTTGGTGTGCTATTCACTGATGGTCAGGAGC 637

Db 1089 CTGCTTTTCTGTGCGCTTTTCCGTAATCCTGGTCTGTGTGCTGTGTGCTGTGTGCTGTG 1148

Qy 638 CTGATCAAGCGAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCGCAGGTCCATC 697

Db 1149 CTGCTCAACCGGCTTATGGGACCAACAGGAGGTCTGCTCGGGCCAAAGTCTGTG 1208

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Db 1209 CGCACCATTCCTTGGTACTGCGCGCTCTTCCGCTCTGCTTCTGCTCTTCCACCTCACG 1268

Qy 758 CGCTCCCTTACCTCACTCACTCTGCTTCTGCTTTCTCAGGACTGCCAGCTCTTGTATGCGCA 817

Db 1269 CGCACCTCTACTACTCTCTCCGAT---CACTTGACCTAGCTGCCACACCTCAACGCC 1325

Qy 818 GCCAGTGTGGCTTACAGATATGGAGGCTCTGCTGCTGTTCTGAGCTGTGAGCAGCTCCCTCAACCCA 877

Db 1326 ATCAACATGGCATATAAGATCACCCGCGCTGCCAGCGCCCAACAGTTGCTGTGACCCG 1385

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**RESULT 4**

CZ014932/c

**LOCUS** CH240 511J04.TJ CHORI-240 Bos taurus genomic clone CH240\_511J04,

**DEFINITION** genomic survey sequence.

**ACCESSION** CZ014932

**VERSION** CZ014932.1 GI:57343493

**KEYWORDS** GSS.

**SOURCE** Bos taurus (cow)

**ORGANISM** Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 271)  
 AUTHORS Costa J.N., Mota M. and Caetano A.R.  
 TITLE Brazil's Contribution to End-Sequencing the Bovine BAC Library  
 JOURNAL CHORI-240  
 COMMENT Unpublished (2003)  
 Other\_GSSs: CH240\_511J04.TV  
 Contact: Caetano AR  
 Department of Biotechnology  
 Embrapa Recursos Geneticos e Biotecnologia  
 Parque Estacao Biologica, Final Av. W/5 Norte, Brasilia-DF C.P.  
 02372, 70770-900 Brasil  
 Tel: 55 61 448 4778  
 Fax: 55 61 340 3658  
 Email: acetano@cenargen.embrapa.br  
 Clones are derived from the bovine BAC library CHORI-240  
 (http://www.chori.org/bacpac/bovine240.html). Bases shown have Phred  
 quality value equal to or higher than 20. Bases with quality value  
 below 20 were masked with 'N'. For BAC library availability, please  
 contact Pieter de Jong (pdejong@mail.cho.org). Clones may be  
 purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/ordering information.htm). This work  
 was undertaken as part of the International Bovine BAC Mapping  
 Consortium (IBBMC) by Embrapa Recursos Geneticos e Biotecnologia  
 with financing from Conselho Nacional de Desenvolvimento Cientifico  
 e Tecnologico (CNPq), Brazil.  
 Plate: 511 row: J column: 04  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence stop: 271.  
 Location/Qualifiers  
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 /cell\_type="Blood"  
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 library (Male) produced by Pieter de Jong"

ORIGIN  
 Query Match 18.1%; Score 181.8; DB 10; Length 271;  
 Best Local Similarity 79.3%; Pred. No. 4.9e-38;  
 Matches 214; Conservative 0; Mismatches 53; Indels 3; Gaps 1;  
 Qy 184 CTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCT---ATTGCCCTTCTCATCATC 240  
 Db |||||  
 270 CTGGGAACCTGATGGTGGCAGATCTGTATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 211  
 Qy 241 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300  
 Db |||||  
 210 ACCTACTCCCTGGAGGACACCTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGGTGGCTTC 151  
 Qy 301 CTGTTCTATATCAACCTTTAGCGGAGCATCTGCTGCTGACCTGCATCTCTGTGCACAG 360  
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 150 CTGTTCTACGCCAACCTCTACAGCAGCGTCTGCTGCTGACCTGCATCTCCGTGCACCGC 91  
 Qy 361 TTCTCTAGGTGTGTCACCACTGTGTTGCTGCTCCCTACCGGACCGCGAGGACGCTCGTGG 420  
 Db |||||  
 90 TTCTTGGGGGTGTGTCACCACTGGCTCTGCTGCTTACCGGACCGCGGACGNNNNNN 31  
 Qy 421 CTGGGACACGACCACTCTGGGCCCTGGTG 450  
 Db |||||  
 30 NNNNNNNNNACCGCCACGTGGGCTCTGGTG 1

RESULT 5  
 CD217676  
 LOCUS  
 DEFINITION pgrin.pk004.g6 Normalized chicken reproductive tract cdna library

(pgrin) Gallus gallus cdna clone pgrin.pk004.g6 5' similar to  
 sp|Q98907|P2Y3.CHICK P2Y purinoceptor 3 (P2Y3) (Nucleoside  
 diphosphate receptor) >emb|CAA66930.1| (X98283) G protein-coupled  
 P2 receptor [Gallus gallus], mRNA sequence.  
 CD217676  
 CD217676.1 GI:30957649  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Gallus gallus (chicken)  
 Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 693)  
 Cogburn L.A. and Nys, Y.  
 Chicken ESTs from reproductive tract  
 Unpublished (2002)  
 JOURNAL  
 COMMENT Contact: Larry A. Cogburn  
 University of Delaware  
 Townsend Hall, Newark, DE 19717, USA  
 Tel: 302-831-1335  
 Fax: 302-831-2822  
 Email: cogburn@udel.edu, www.chickest.udel.edu.  
 Location/Qualifiers  
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 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Commercial broiler and layer"  
 /db\_xref="taxon:9031"  
 /clone="pgrin.pk004.g6"  
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 /dev\_stage="Various stages; embryonic, post-hatch, immature  
 and sexually-mature"  
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 library (pgrin)"  
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 RNA pools from each tissue (testis 25%, ovary 25%, and  
 oviduct 50% of final RNA pool) Single pass sequencing from  
 5'-end"

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 Best Local Similarity 59.4%; Pred. No. 3.2e-37;  
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 Qy 43 TGCCAGTTCTCAGAGAAGTACAGCAAGTCTACTCTCCCTGGCCTACAGTATCATCTTT 102  
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 67 TGCACCTTCCATGAGGAATTCAGCAGGTCTCTGCGCCCTGGTCTACTCAGTGGTGTTC 126  
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 Db |||||  
 127 CTACTGGGGCTGCCACTCAATGCGGTGTCTATGGGAGATCTGGCTGGCCCGCAAGCGC 186  
 Qy 163 TGGAGCTGTGTGCCACCACTATCTGGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTA 222  
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 187 TTGACCCGCAACCACTATCATGCTGAACCTGGCCATGGCCGACCTGCTTTATGTCTGC 246  
 Qy 223 T---TGCCCTTCTTCATCATCCTACTCATAGATGACAGGTGGCCCTTCGGGGAGCTG 279  
 Db |||||  
 247 TCCCTCCCTCTCTCTCATCTACAATACACCCAGGAAGATTACTGGCCCTTTGGGACTTC 306  
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 Db |||||  
 307 ACCTGCAAAATTCGTCGCCGCTTCCAGTCTTACACCAACCTGACCGGAGCATCTCTTCTC 366  
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 Db |||||  
 367 ACCTGCAATCAGCGTCCAGCGCTACATGGGATCTGCCACCCCTTTGGCCTCTGTCACAA 426  
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Qy 457 CAGCTGTGCCACACTGGGCTTCTCCACACGAGACTACATCAATGGCCAGATGATCTGG 516
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Qy 635 AGCCTG 640
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Db 667 ATCCTG 672
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RESULT 6
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LOCUS
DEFINITION
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genomic survey sequence.
ACCESSION
DQ052984
VERSION
DQ052984.1
KEYWORDS
GI:66898931
SOURCE
GSS.
ORGANISM
Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE
1. (bases 1 to 1073)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
(Preprint) PLoS Biol. 3 (6), E170 (2005)
2. (bases 1 to 1073)
Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D.,
White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
FEATURES
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location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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/gene="P2RY2"
/locus_tag="HC13517"

gene
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Matches 367; Conservative 0; Mismatches 486; Indels 8; Gaps 3;

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43 TGGCAGTTCTCAGAGAAAGTACAAGCAAGTCTTACCTCTCCCTGGCCTACAGTATCATCTTT 102
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Db 28 TGCNNNTCAACGAGGACNTCAAGTACNNNTCTGCTGCTGTNTCNACGGGTGTGT 87
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Db 88 GTGCTGGGCTGTGNNNGAAGCGCGCTGCGNNNNNCAANNNTCNTGTNNNNNCAAGANC 147
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Qy 460 CTGCTGCCACACTGGGCTTCTCCACACGACATACATCAATGGCCAGATGTGTAT 519
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Db 448 CAGGCGCGCGCTGCGNNACTTTGTNNNNNCCAGCGCGCGGGGCGCGNNNTAACTGCCAC 507
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Qy 520 GACATGACCAAGCAAGAGAAATTTTGATCGGCTTTTTCCTTACGCGCATAGTCTGACATTG 579
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Db 508 NACANCNNGNACCCGAGCANNNTCAGCGCNNNNNNNNNNNNNNNNNNNNNNNNNNNN 567
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Qy 818 GCAGTGTGGCTTACAGATATGAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCA 877
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Qy 878 GTCTGTACTTTCTTTCAAGG 898
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Db 865 GTGCTTACTTCTTGGCTGG 885
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RESULT 7
AY400797
LOCUS
DEFINITION
Homo sapiens P2RY6 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION
AY400797
VERSION
AY400797.1
KEYWORDS
GI:39756786
SOURCE
GSS.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE
1. (bases 1 to 987)
Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
JOURNAL
PUBMED
14671302

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Qy 279 GCTCTGCAAGCTGGTGCACCTTCCTGTTCTATATCAACCTTTACGGCAGCATCTCTGCTGCT 338
Db 464 CGCTGCGCGCTGGTGCCTGCTCTCTTCTATGCAACCTTCACGGCAGCATCTCTCTCT 523
Qy 339 GACCTGATCTCTGTGCACAGTTCCTAGGTGTGTGCACCCACTGTGTTCGCTGCGCCTA 398
Db 524 CACCTGATCAGTTCCTCAGGGCTACCTGGGCACTGTGCACCCGCTGGCCCTGGGCAAA 583
Qy 399 CC---GGACCGCAGGATGCTGGCTGGGACACAGCACCACCTGGGCCCTGTGTGTCCT 455
Db 584 ACGTGGGGCGCGCGGCTGCTGGCTAGTGTGTGTAGCGGTGTGGCTGGCGGTGACAAC 643
Qy 456 CCAGCTGCTGCCACACTGGCTTCTCCACACGGACTACATCAATGGCCAGATGATCTG 515
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Qy 516 GTATGACATACACAGCAAGAGATTTTGTATGGCTTTTGGCTTACGGCATAGTTCGTAC 575
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Qy 576 ATTGTCTGGCTTCT--TTCCCTCTTGGTCAATTTTGGTGTGCTATTACTGATGTGTGCTG 633
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Qy 694 CATCGGACCATCTACTGTGTGTGGCTTTCACCTCTGTGTTTGTGGCTTCCATAT 753
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Qy 814 GGCAGCAGTGTGCGCTACAGATATGAGGCTCTGCTGAGTGTGAGAGCTGCGCTCAA 873
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Db 1064 CCCATCTCTTCT 1077
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RESULT 9
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LOCUS full-length cDNA clone CSODI044YA15 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR612681
VERSION CR612681.1 GI:50493488
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1515)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1515)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequenage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

## FEATURES

## source

## Location/Qualifiers

1. .1515  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CSODI044YA15"  
/tissue\_type="Placenta Cot 25-normalized"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

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Query Match 16.4%; Score 164.8; DB 4; Length 1515;
Best Local Similarity 52.0%; Pred. No. 3.3e-33;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

Qy 42 CTGCCAGTTCTCAGAGAAGTACAAAGTCTACCTCTCCCTGCGCTTACAGTATCATCTT 101
Db 312 CTGTGCTACCGGAGAACTTCAAGCAACTGTGCTGCCACCTGTGTATTTCGGGGTGTCT 371
Qy 102 TATCTAGGGCTGCCACTAAATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
Db 372 GCGGGCTGGCTGCGCTGAACATCTGTGTCAATACCCAGATCTGCACGTCCTCCGCGGGC 431
Qy 162 CTGGAGTGTGCCACACCACTATCTGTGTGAACCTGTATGTGGCGACCTGTCTTTATGTGCT 221
Db 432 CTTGACCCGACGCGCGGTGTACACCCCTAAACCTTTGCTCTGGCTGACCTGTATATGCTG 491
Qy 222 AT---TGCCCTTCTCATCATCACTACTCATCTAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db 492 CTCCTTGGCCCTGCTCATCTACAACTATGCCAAGGTGATCACTGGCCCTTTGGCGACTT 551
Qy 279 GCTCTGCAAGCTGGTGCACCTTCTCTTCTATATCAACCTTTACGGCAGCATCTCTGTGCT 338
Db 552 CGCTGCGCGCTGGTTCGCTTCTCTTATGCAACCTGCACGGCAGCATCTCTTCTCT 611
Qy 339 GACCTGATCTCTGTGACACAGTTCCTAGTGTGTGGCAACCACTGTGTTCGCTGCGCTA 398
Db 612 CACCTGATCAGCTTCAGCGCTACCTGGGCATCTGCCACCCGCTGGCCCTGGGCAAA 671
Qy 399 CC---GGACCCGAGGATGCGCTGGCGTGGCACACAGCACCTGGCCCTGTGTGCTCT 455
Db 672 ACGTGGGGCGCGCGGCTGCTGCTGCTGTGTGTAGCGGTGTGGCTGGCCGTGACAAC 731
Qy 456 CCAGCTGCTGCCACACACTGGCTTCTCCACACGGACTACATCAATGGCCAGATGATCTG 515
Db 732 CCAGTGGCTGCCACAGCCATCTTCGTGCAACAGGATCCAGGTAACCGCACTGTCTG 791
Qy 516 GTATGATGACAGCAGCCAGAGAAATTTTGTATGCGCTTTTGGCTACCGCATAGTCTTGAC 575
Db 792 CTATGACCTCAGCCCGCTGCGCTGCCCTGACCCACTATATGCCCTATGCGCATGGCTCTCAC 851
Qy 576 ATTGTCTGGCTTCT--TTCCCTTCTTGGTCAATTTTGGTGTGCTATTACTGATGTGTGCTG 633
Db 852 TGTATCGGCTTCTGCTGCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 911
Qy 634 GAGCTGATCAAGCAGAGAGAGAACTCATGAGGACAGGCAACACAGCCCGAGCAGGTC 693
Db 912 CCGCTGTGCGCGAGGATGGCCCGGAGAGCCCTGTGGCCAGGAGCGGTGCGCAAGGC 971
Qy 694 CATCCGAGCATCTCTACTGTGTGTGGCTCTTTCACCCCTGTGTTTGTGGCTTCCATAT 753
Db 972 GGGCCGATGGCGGTGTGTGGCTGTGCTTTTGGCATCAGCTTCTGCTGCTTTTTCAT 1031
Qy 754 CACTGCTCTTCTACTCATCATCTGCTTCTTCTGCTTCTCAGGACTGCCAGCTCTTGAT 813
Db 1032 CACCAAGACAGCTTACTGTGCACTGCGCTCGAGCGCGGCGTCCCTGTGCACTGTATTGGA 1091
Qy 814 GGCAGCAGTGTGGCTTACAGATATGAGGCGCTCTGGTGTGTGTGTGAGCAGCTGCTCAA 873
Db 1092 GGCCTTTGACGCGCTTACAAAGCACGCGCGCTTTGCGAGTGCCAAACAGCGGTGTGA 1151
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Qy 874 CCCAGTCTCTACT 887
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Db 1152 CCCATCTCTTCT 1165

RESULT 10
CR618945 1532 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI042YA16 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR618945
VERSION CR618945.1 GI:50499752
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 1532)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
REFERENCE 2 (bases 1 to 1532)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefgenoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
FEATURES             Location/Qualifiers
     source           1..1532
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CSODI042YA16"
                     /tissue type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"

ORIGIN
Query Match      16.4%; Score 164.8; DB 4; Length 1532;
Best Local Similarity 52.0%; Pred. No. 3.3e-33;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;

Qy 42 CTGCAGTTCAGAGAGTACAGCAAGTCTACTCTCTCCCTGGCCTACAGTATCATCTT 101
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Db 312 CTGTGTCTACCGCGAGAACTTCAAGCAACTCTGCTGCCACCTGTGTATTCCGGCGGTGCT 371
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Qy 102 TATCTAGGGTGCACCTAAATGGCACTGCTTGTGGCACTTCTGGGCGCCAAACCAAGCG 161
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Db 372 GCGGCTGGCTGCGCTGACATCTGTGTATACCAGATCTGCAGTCCGCGCGGC 431
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Qy 162 CTGGAGCTGTGCCACCACTATCTGTGGTGAACCTGTATGGTGGCGCACTGCTTTATGTGCT 221
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Db 432 CCGTACCGCGACGCGGTGTACACCTAAACCTTGCTCTGGCTGACCTGCTATATGCTG 491
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Qy 222 AT---TGGCCTTCCTCATCATCACTACTCTAGATGACAGGTGGCCCTTGGGGGAGCT 278
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Db 492 CTCCCTGCCCTGCTCATCACTAAGTATGCCCAAGGTGATCACTGGCCCTTTGGCGACTT 551
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Qy 279 GCTCTCAAGCTGGTCACTTCTCTTCTATATCAACTTTAGCGCAGCATCTGCTGCT 338
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Db 552 GCGCTGCCGCTGGTCCGCTTCTCTTCTATGCCAACTGACGCGCAGCATCTCTTCTCT 611
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Qy 339 GACCTGCATCTCTGTGCACCAAGTTCCTAGGTGTGTGCCACCACTGTGTGCTGCCCTA 398
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Db 612 CACCTGCATCAGCTTCCAGCGCTACCTGGGCATCTGCCACCGCTGGCCCTCGSCACAA 671
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Qy 456 CCAGCTGCTGCCACACACTGGCCCTTCTCCACACAGGACTACATCAATGAGCCAGATGATCTG 515
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Db 732 CCAGTGGCTGCCACAGCCATCTTTCGCTGCGCACAGGCACTCCAGCGTAACCGCACTGTCTG 791
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Qy 516 GTATGACATGACAGCAAGAGATTTTGTATGCGCTTTTGGCTTACGCGATAGTCTTGAC 575
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Db 792 CTATGACCTCAGCCGCGCTGCCCTGGGCACCACTATATGCCCTATGCGATGGCTCTCAC 851
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Qy 576 ATTGTCTGGCTTCT---TTCCCTCTCTTGGTCAATTTTGGTGTGCTATTCACTGATGGTCTG 633
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Db 852 TGTATCGGCTTCTGCTGCGCTTGTGCGCTGCTGGCTGCTACTGTCTCTCGGCTG 911
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 634 GAGCCTGATCAAGCCAGAGGAGAACTCATGAGGACAGGCAACAGAGCCCGAGCCAGGTC 693
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Db 912 CCGCTGTGCGCGCAGGATGGCCGCGAGAGCCTGTGGCCAGGAGCGCGTGGCAAGGC 971
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Qy 694 CATCGGACCATCTACTGTGTGGCTCTTCAACCTCTGTTTGTGGCCCTTCCATAT 753
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Db 972 GCGCCGATGCGCTGTGTGGCTGTGCTTGGCCATCAGCTTCTGCTCTTTTCAT 1031
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Qy 754 CACTCGCTCTTCTACCTCACCATCTGCTTCTCTTCTCAGGACTGCCAGCTCTTGAT 813
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Db 1032 CACCAAGACAGCCTACTCTGGCAGTGCCTCGACGCGGGCGTCCCTGCACTGATTGA 1091
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Qy 814 GGCAGCCAGTGTGGCTTACAGATATGAGAGCCTCTCGTGTAGTGTGAGCAGCTGCCCAA 873
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Db 1092 GGCCTTTGACGCGCCTACAAAGGCACGCGGCCCTTTGCCAGTGCCAAACGCGTCTGA 1151
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Qy 874 CCCAGTCTCTACT 887
    ||| ||| ||| |||
Db 1152 CCCATCTCTTCT 1165
    ||| ||| ||| |||

RESULT 11
CR626266 1564 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSODI038YC15 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR626266
VERSION CR626266.1 GI:50507073
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 1564)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
REFERENCE 2 (bases 1 to 1564)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefgenoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
FEATURES             Location/Qualifiers
     source           1..1564
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
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LOCUS	CR626754	1589 bp	mRNA	linear	HTC 21-JUL-2000
DEFINITION	full-length cDNA clone CS0DI024YE14 of Placenta Cot 25-normalized of Homo sapiens (human).				
ACCESSION	CR626754				
KEYWORDS	HTC; CNSLT_cDNA.				
SOURCE	CR626754.1 GI:50507616				
ORGANISM	Homo sapiens (human)				
REFERENCE	1. (bases 1 to 1589)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2. (bases 1 to 1589)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)				
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1. .1589				
	/organism="Homo sapiens"				
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	/db_xref="taxon:9606"				
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	/issue_type="Placenta Cot 25-normalized"				
	/plasmid="pCMVSPORT_6"				
ORIGIN					
Query Match	16.4%;	Score 164.8;	DB 4;	Length 1589;	
Best Local Similarity	52.0%;	Pred. No. 3.3e-33;			
Matches	444;	Conservative	0;	Mismatches 402;	Indels 8; Gaps 3;
Qy	42	CTGCCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCGCTACAGTATCATCTT	101		
Db	343	CTGTGTCTACCGGAGAACTTCAAGCAACTGTCTGCCACCTGTGTATTTCGGCGGTCT	402		
Qy	102	TATCCTAGGCTGCACATAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG	161		
Db	403	GGCGCTGGCTGGCGCTGNAACATCTGTGTCAATTACCCAGATCTGCAGTCCCGCGGCG	462		
Qy	162	CTGGAGCTGTGCCACCACTTATCTGTGTGAACCTGATGTGTGGCGGACCTGTTATGTGCT	221		
Db	463	CCTGACCGCACGGCGGTGTACACCCCTAAACCTTGTCTGTGGCTGCTATATGCGCTG	522		
Qy	222	AT---TGCCCTTCTCATCATCACTACTCACTAGATGACAGTGGCCCTTCGGGAGCT	278		
Db	523	CTCCCTGCCCTGCTCATCTACAACTATGCCAAGGTATCACTGGCCCTTTGGGCACTT	582		
Qy	279	GCTCTGAAGCTGTGCACCTCTCTGTCTTATATCAACCTTTACGCGACGATCCTGCTGCT	338		
Db	583	CGCCTGGCGCTGTGCGCTTCTCTTCTATGCGCAACCTGCAAGGAGATCCTCTTCTCT	642		
Qy	339	GACCTGCATCTCTGTGCACAGTTCCTTAGTGTGTGCCACCCACTGTGTTCGTCGCCCTA	398		
Db	643	CACCTGCATCAGCTTCCAGCGCTACCTGGGCACTTGCACACCGCTGGCCCTCGSCACAA	702		
Qy	399	CC---GGACCGGAGGATGCTCGCTGGCGCACGACCACTCGGCGCCCTGGTGTCTCT	455		
Db	703	ACGTGGGGCGCGCGGCTGCTGGCTAGTGTGTGTAGCCGTGTGGCTGGCGCTGACAA	762		
Qy	456	CCAGCTGCTGCCACACTGCGCTTCTCCACAGGACTATACATCAATGGCCAGATGATCTG	515		
Db	763	CCAGTGCCTGCCACAGCCATCTTCGCTGCCACAGGATCCAGGCTAACCGCACTGTCTG	822		
Qy	516	GTATGACATGACGACCAAGAGAAATTTGATCGGCTTTTTCCTACCGCATATGTTCTGAC	575		
Db	823	CTATGACCTCAGCCCGGCTGCGCTGGCCACCCACTATATGCCCTATGGCATGGCTCTCAC	882		
Qy	576	ATTGCTCGGCTTCTCT--TTCCCTCTTGGTCACTTTTGGTGTGCTATTACTAGTGTGAG	633		
Db	883	TGTCATCGGCTCTGCTGTCGCTTTCCTGCGCTGCTGGCTGCTACTGTCTCTCTGGCTG	942		
Qy	634	GAGCTGATCAAGCAGAGGAGAACCTCATGAGGACAGGACACACAGCCCGGACGAGTGC	693		
Db	943	CGGCTGTGCGGCAGGATGGCCCGGAGAGCGCTGTGGCCAGGAGCGCGTGGCAAGGC	1002		
Qy	694	CATCCGACCATCTACTGTGTGTGGCTCTTTCACCTCTGTCTTGTGGCCCTTCCATAT	753		
Db	1003	GGCCCGCATGGCGGTGTGTGTGCTGTGCTTGGCATGACGTTCTCTGCTTTTCAT	1062		
Qy	754	CATCGCTCTTTTACTCAACATCTGCTTTCTGCTTTTCTCAGGACTGCGAGCTCTTGAT	813		
Db	1063	CACCAAGACAGCTTACCTGTCAGTGGCTCGAGCGCGGCGCTCCCTGCACTGTATTGGA	1122		
Qy	814	GGCAGCAGTGTGGCTTACAGATATGGAGGCTCTGTGTAGTGTGAGCAGCTGGCTCAA	873		
Db	1123	GGCTTTTTCAGCGGCTTACAAAGGCAACGCGGCGGCTTTGCCAGTGGCAACAGCGTCTGGA	1182		
Qy	874	CCAGTCTCTTACT	887		
Db	1183	CCCACTCTCTCT	1196		
ORIGIN					
Query Match	16.4%;	Score 164.8;	DB 4;	Length 1564;	
Best Local Similarity	52.0%;	Pred. No. 3.3e-33;			
Matches	444;	Conservative	0;	Mismatches 402;	Indels 8; Gaps 3;
Qy	42	CTGCCAGTTCTCAGAGAGTACAGCAAGTCTACCTCTCCCTGGCGCTACAGTATCATCTT	101		
Db	343	CTGTGTCTACCGGAGAACTTCAAGCAACTGTCTGCCACCTGTGTATTTCGGCGGTCT	402		
Qy	102	TATCCTAGGCTGCACATAAATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCG	161		
Db	403	GGCGCTGGCTGGCGCTGNAACATCTGTGTCAATTACCCAGATCTGCAGTCCCGCGGCG	462		
Qy	162	CTGGAGCTGTGCCACCACTTATCTGTGTGAACCTGATGTGTGGCGGACCTGTTATGTGCT	221		
Db	463	CCTGACCGCACGGCGGTGTACACCCCTAAACCTTGTCTGTGGCTGCTATATGCGCTG	522		
Qy	222	AT---TGCCCTTCTCATCATCACTACTCACTAGATGACAGTGGCCCTTCGGGAGCT	278		
Db					



Db	802	CCAGTGCCTGCCCA	CAGGCATCTCTCGCTGCCA	CAGGCATCCAGCGTAACCGCACTGTCTG	861
Qy	516	GTATGACATGACAC	CAAGAGAATTTTGATCGGCTTTTGCCCTACGGCATAGTTCTGTAC	575	
Db	862	CTATGACCTAGCCG	CGGCTGCCCTGGCCACCCACTATATGCCCTATGGCATGGCTCTCAC	921	
Qy	576	ATTGCTGGCTTCT	--TTCCCTCCTTGGTCAATTTGGTGCTGCTATTCACTGATGGTCTAG	633	
Db	922	TGTCATGGCTTCT	CTGTGCTGCTTTGCTGCCCTGCTGCTACTGCTCTCTCTCGTGGCCTG	981	
Qy	634	GAGCCTGATCAAG	CCAGGAGAACTCATGAGGACAGGCAACACAGCCCGAGCCAGTCT	693	
Db	982	CCGCTGTGCGCG	CAGGATGSCCCGGCAGAGCCTGTGCCCAGGAGCGGCTGGCAAGGC	1041	
Qy	694	CATCCGACCATCT	ACTGCTGTGGCTCTTCACCTCTGTTTGTGCGCTTTCCTATAT	753	
Db	1042	GGCCCGCATGSCG	TGGTGCTGCTGCTTTTGCCATCAGCTTCCTGCTCTTTCACAT	1101	
Qy	754	CACTCGCTCCTT	CTACCTCACCATCTGTGTTTCTGCTGTTTCTCAGGACTGCCAGCTCTTGAT	813	
Db	1102	CACCAAGACAGCT	TACCTGGCAGTGCCTGACGCCGGGCTCCCTGCACTGTATTGGA	1161	
Qy	814	GGCAGCAGTGTGC	CGCTACAAGATATGGAGCCCTCTGCTGAGTGTGAGCAGCTGCCCTCAA	873	
Db	1162	GGCCCTTTGACG	CGSCCTACAAAGCAGCGCGCCGTTTGCCAGTGCCCAACAGCGTCTGGA	1221	
Qy	874	CCAGTCTCTGTACT		887	
Db	1222	CCCCATCTCTTCT		1235	

**RESULT 13**  
**LOCUS** CR605588 1592 bp mRNA linear HTC 21-JUL-2004  
**DEFINITION** full-length cDNA clone CSODI040YB02 of Placenta Cot 25-normalized of Homo sapiens (human).  
**ACCESSION** CR605588  
**VERSION** CR605588.1 GI:50486395  
**KEYWORDS** HTC; CNSUT\_cDNA.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 1592)  
Li, W.B., Gruber, C., Jeasee, J. and Polayes, D.  
**AUTHORS** Full-length cDNA libraries and normalization  
**TITLE** Unpublished  
**JOURNAL** Contact : Feng Liang Email : fliang@lifetech.com URL :  
**REMARK** http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue  
2 (bases 1 to 1592)  
Genoscope.  
**REFERENCE** Direct Submission  
**AUTHORS** Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
**JOURNAL** BP 191 91006 EVRY cedex - FRANCE (E-mail : secre@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr)  
**COMMENT** 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.  
**FEATURES** Location/Qualifiers  
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1..1592  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/tissue\_type="Placenta Cot 25-normalized"  
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**ORIGIN**  
Query Match 16.4% Score 164.8; DB 4; Length 1592;

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1594)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1594)
Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES             Location/Qualifiers
     source           1..1594
                     /organism="Homo sapiens"
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                     /tissue_type="Neuroblastoma Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN
Query Match       16.4%; Score 164.8; DB 4; Length 1594;
Best Local Similarity 52.0%; Pred. No. 3.3e-33;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;
Qy 42 CTGCCAGTTCTCAGAGATACAGCAAGTCACTCTCCCTGCGCTACAGATATCATCTT 101
Db |||
Qy 371 CTGTGTTACCGCGAGAACTTCAAGCAACTGCTCTGCCACCTGTGATTGGCGGTCT 430
Db |||
Qy 102 TATCCTAGGCTGCCACTTAATGGCACTGCTTGTGGCACTTCTGGGCGCAAAACCAAGCG 161
Db |||
Qy 431 GGCGGTGGCTGCGGTGACATCTGTGTGTCATACCAAGATCTGACGTCGCCCGCGGC 490
Db |||
Qy 162 CTGAGCTGTGCCACCACTATCTGTTGAACCTGATGGTGGCGCACTGCTTTATGTGCT 221
Db |||
Qy 491 CCTGACCGGACGCGCTGTACACCTTAACTTGTCTGGCTGACCTGTATATGCTG 550
Qy 222 AT---TGGCCTTCCTCATCATCACTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
Db |||
Qy 551 CTCCTGCCCCCTGCTCATCTACAACTATGCCCCAAGGTGATCACTGGCCCTTTGGCGACTT 610
Qy 279 GCTCTGAAGCTGGTGCACTTCTGTTCTATATCAACTTTTACGGCAGCATCTGCTGCT 338
Db |||
Qy 611 CGCTGCGGCTGGTCTGCTTCTTCTATGCAACTGCAAGGAGATCTCTCTCT 670
Qy 339 GACCTGATCTCTGTGACCAAGTTCCTAGGTGTGTGCCACCACTGTGTCGTGCCCTA 398
Db |||
Qy 671 CACCTGATCAGCTTCCAGCGCTACCTGGGATCTGCCACCGCGCTGGCCCTGGCACAA 730
Qy 399 CC---GGACCGGAGGATGCTGGCTGGGACACAGCACCACTGGCCCTTGGTGTCTCT 455
Db |||
Qy 731 ACGTGGGGGCGCGGGCTGCTGGCTAGTGTGTGTAGCCGTGTGGCTGGCCGTGACAAC 790
Qy 456 CCAGCTGTGCGCCACACTGGGCTTCTCCACACGAGCTACATCAATGGCCAGATGATCTG 515
Db |||
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Db |||
Qy 851 CTATGACTCAGCCCGGCTGCGCTGCCACCACTATATGCGCTATGCGATGGCTCTCAC 910
Qy 576 ATTGCTGGCTTCT--TTCCCTCTTGGTCATTTGGTGTGCTATTCACTGATGGTCAG 633
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Db 1091 CACCAAGACAGCCTTACTTGGCAGTGGCTCGACGCGCGGCGTCCCCTTGCACTGTATTGGA 1150
Qy 814 GGCAGCCAGTGTGGCTTACAAAGATATGAGAGCCTCTGGTGAGTGTGAGCAGCTGCCTCAA 873
Db 1151 GGCTTTGACAGCGCTTACAAAGGACGCGCGCTTTGGCAGTGGCCACAGCGGTGCTGGA 1210
Qy 874 CCAGTCTCTTACT 887
Db 1211 CCCATCCTCTTCT 1224
RESULT 15
CR617080 1638 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DI040YPI7 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CR617080.1 GI:50497887
VERSION HTc; CNSLT_cDNA.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1638)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
Genoscope.
2 (bases 1 to 1638)
Direct Submission
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES             Location/Qualifiers
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                     /clone="CS0DI040YPI7"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN
Query Match       16.4%; Score 164.8; DB 4; Length 1638;
Best Local Similarity 52.0%; Pred. No. 3.4e-33;
Matches 444; Conservative 0; Mismatches 402; Indels 8; Gaps 3;
Qy 42 CTGCCAGTTCTCAGAGATACAGCAAGTCACTCTCCCTGCGCTACAGATATCATCTT 101
Db |||
Qy 415 CTGTGCTACCGGAGAACTTCAAGCAACTGCTGCTGCCACCTGTGTATTTCGGGGTCT 474
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Qy 102 TATCTAGGGCTGCCAATAATGGCACTGTCTTTGTGGCACTTCTGGGGCCAAACCAAGCG 161
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 475 GCGGCTGGCCCTGCCGCTGAACATCTGTGTATACCCAGATCTGCACTCCCGCGGCG 534
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 162 CTGGAGCTGTGCCACCACTATCTGGTGAACTGTATGGTGGCCGACCTGCTTTATGTGCT 221
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 535 COTGACCCGCGAGGCGGTATACCCCTAAACCTTCTCTGGCTGACCTGCTATATGCTG 594
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 222 AT---TGCCCTTCCCTCATCATCACTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCT 278
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Qy 595 CTCCCTGCCCTTGTCTATCTCACTATGCCCAAGGTGATCACTGGCCCTTTGGGACTT 654
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 279 GCTCTGAAGCTGTGCACTTCTCTCTTATATCAACCTTTACGGCAGCATCCTGCTGCT 338
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Qy 655 CGCTGGCCGCTGGTCCGCTTCTCTATGSCCAACCTGCACGGCAATCCTCTTCT 714
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Qy 339 GACCTGATCTGTGTGCAACCACTTCTAGGTGTGTGCCACCACTGTGTTCGCTGCCCTA 398
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Qy 715 CACCTGATCACTTCCAGCGCTACCTGGGCACTCTGCCACCGCTGGCCCTTGGCAAA 774
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Qy 516 GTATGACATGACCAAGCAAGAAATTTTGTATGGGCTTTTGTGCTACGGCATAGTTCGAC 575
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Qy 576 ATTGCTGCTTCTTCT---TTCCCTCTTGTGTCTATTTTGTGTGTCTATTCACTGATGCTCAG 633
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 955 TGTATCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1014
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 634 GAGCTGATCAAGCCAGAGGAGAACCTCATGAGGACAGGCAACACAGCCCGAGCCAGGTC 693
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1015 CCGCTGTGCCCGCAGGATGGCCCGGAGAGCCTGTGCCCCAGGAGCGGCGTGGCAAGGC 1074
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Qy 754 CACTGCTCTCTTCTACTCACTCACTCTCTTCTGCTTCTCAGGACTGCCAGCTCTTGAT 813
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1135 CACCAAGACAGCCTACCTGGCAGTGCCTCGACGCGGGCGTCCCTGCACTGTATTGGA 1194
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 814 GCGAGCCAGTGTGGCTTACAAGATATGAGGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 873
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1195 GGCCTTTGAGGGGCTTACAAGGACACGGGCGGTTTGCCAGTGCCAAACAGGTGCTGGA 1254
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Qy 874 CCCAGTCTCTACT 887
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Job time : 4767 secs

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OM nucleic - nucleic search, using sw model

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1002	100.0	1002	4	Aah73516 Human G p
2	1000.4	99.8	1156	10	Adb99267 Human p2Y
3	1000.4	99.8	1334	10	Adc86166 Human GPC
4	1000.4	99.8	3143	6	Aas17746 Human gen
5	996.4	99.4	1082	6	Abq76000 Human GPC
6	983.4	98.1	1063	6	Aas98135 Human DNA
7	977.4	97.5	1108	6	Adi16629 Human NOV
8	977.4	97.5	1108	12	Adn42283 Human CDN
9	920.4	91.9	1017	10	Adc25999 Human pur
10	920.4	91.9	1017	10	Aad61648 Human GPC
11	917.2	91.5	1020	6	Abq79300 Human GPC
12	917.2	91.5	1076	6	Aad29667 Human G-p
13	917.2	91.5	1076	12	Ado30395 Human GPC
14	848.4	84.7	850	6	Aas17747 Human p2Y
15	604.6	60.3	906	12	Ado30397 Mouse GPC
16	510	50.9	510	6	Aah50975 Human nGP
17	510	50.9	510	6	Abq70208 DNA encod
18	400.4	40.0	681	4	Aas30774 Human CDN
19	374	37.3	585	4	Aas30783 Human CDN

20	237.4	23.7	1163	12	ADP49190	Adp49190 Chick p2Y
21	229.4	22.9	1134	12	ADO30017	Ado30017 Human GPC
22	229.4	22.9	2025	4	AAO04980	Aao04980 Human pur
23	229.4	22.9	2025	6	ABZ35611	Abz35611 Human gen
24	229.4	22.9	2025	8	ABZ42713	Abz42713 Human pur
25	229.4	22.9	2025	10	ACA56884	Aca56884 Human sig
26	229.4	22.9	2025	12	ADI56680	Adi56680 Human pol
27	229.4	22.9	2025	12	ADP49188	Adp49188 Human p2Y
28	227.8	22.7	2118	6	ABZ35320	Abz35320 Human gen
29	226.2	22.6	2547	12	ADP21380	Adp21380 Gene p2RY
30	225.2	22.5	1163	4	AAO04981	Aao04981 Human pur
31	203.8	20.3	1122	12	ADO30307	Ado30307 Mouse GPC
32	203.8	20.3	1842	2	AAQ88134	Aaq88134 Human p2O
33	203.8	20.3	2138	6	AAO32944	Aao32944 Mus muscu
34	203.8	20.3	2138	6	AAO32937	Aao32937 Mus muscu
35	189.4	18.9	2011	10	ADB52840	Adb52840 Primary r
36	189.4	18.9	2011	13	ADV41117	Adv41117 Rat cardi
37	180.2	18.0	1098	8	ABZ42771	Abz42771 Human pyr
38	180.2	18.0	1098	12	ADO30018	Ado30018 Human GPC
39	180.2	18.0	1428	12	ADP21381	Adp21381 Gene p2RY
40	180.2	18.0	1429	2	AAO74321	Aao74321 Human p2Y
41	180.2	18.0	1429	10	ACA56470	Aca56470 Human sig
42	180.2	18.0	1429	12	ADI56266	Adi56266 Human pol
43	180.2	18.0	1429	12	ADP49192	Adp49192 Human p2Y
44	175.4	17.5	1651	10	ADE40462	Ade40462 Human pyr
45	170	17.0	234	4	AAS30782	Aas30782 Human CDN

ALIGNMENTS

RESULT 1  
AAH73516  
ID AAH73516 standard; DNA; 1002 BP.

XX AC AAH73516;  
XX AC  
DT 25-SEP-2001 (first entry)  
XX DE Human G protein-coupled receptor GPRV71 coding sequence.  
XX KW Human; guanosine triphosphate binding protein-coupled receptor;  
KW GPRV47; GPRV51; GPRV71; GPRV72; cancer; liver cirrhosis;  
KW Alzheimer's disease; cytostatic; hepatotropic; neurotropic;  
KW neuroprotective; gene therapy; peptide therapy; db.  
XX OS Homo sapiens.  
XX OS  
PN WO200148188-A1.  
XX PD 05-JUL-2001.  
XX PF 28-DEC-2000; 2000WO-JP009408.  
XX PR 28-DEC-1999; 99JP-00375152.  
XX PR 31-MAR-2000; 2000JP-00101339.  
XX PA (HELI-) HELIX RES INST.  
XX PI Matsumoto S, Oda T, Saito Y, Morikawa N, Yoshida K, Suwa M;  
PI Sugiyama T, Kishimoto T, Kanzaki K, Yasuda S, Inoue Y;  
XX WPI; 2001-425662/45.  
XX P-PSDB; AAG64125.  
XX PT New DNA encoding guanosine triphosphate binding protein coupled receptors  
XX PT and their expression products for screening potential anticancer and  
XX PS neurotropic drugs and in diagnosis of these diseases.  
XX Example 1; Page 142-143; 170pp; Japanese.  
XX The invention relates to nine human guanosine triphosphate binding

CC protein (G protein)-coupled receptors designated GPRv8, GPRv12, GPRv16,  
CC GPRv21, GPRv40, GPRv47, GPRv51, GPRv71 and GPRv72, and to the genes  
CC encoding them. These genes and proteins and antibodies against the  
CC protein are useful in the treatment, prevention, diagnosis and  
CC investigation of diseases associated with G protein-coupled receptors,  
CC including cancer, cirrhosis of the liver and Alzheimer's disease. The  
CC present sequence is a G protein-coupled receptor coding sequence of the  
CC invention  
XX  
SQ Sequence 1002 BP; 207 A; 293 C; 249 G; 253 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1002; DB 4; Length 1002;  
Best Local Similarity 100.0%; Pred. No. 7.4e-263;  
Matches 1002; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGAGAGAGGTGGACATGATATACATACAGGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 60  
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Qy 61 TACAAGCAAGTCTACCTCTCTGCGCTTA CAGTATCATCTTTATCTTAGGGCTGCCACTA 120  
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Qy 121 AATGGCACTGCTTTGTGCACTCTCTGGGCGCAACCAAGCGCTGGAGCTGGCCACCACC 180  
Db 121 AATGGCACTGCTTTGTGCACTCTCTGGGCGCAACCAAGCGCTGGAGCTGGCCACCACC 180  
Qy 181 TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 240  
Db 181 TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 240  
Qy 241 ACCTACTCATAGATGACAGTGGCCCTTGGGAGCTGCTTCGCAAGCTGGTGCACTTC 300  
Db 241 ACCTACTCATAGATGACAGTGGCCCTTGGGAGCTGCTTCGCAAGCTGGTGCACTTC 300  
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGACCTGCATCTCTGTGSCACAG 360  
Db 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGACCTGCATCTCTGTGSCACAG 360  
Qy 361 TTCTTAGGTGTGTCACCCACTGTTGCTGCGTCCCTACCGGACCGCAGGCAATGCCCTG 420  
Db 361 TTCTTAGGTGTGTCACCCACTGTTGCTGCGTCCCTACCGGACCGCAGGCAATGCCCTG 420  
Qy 421 CTGGGCAACGACACACTGGGCCCTCTGAGTCTCTCCAGTGTGCTGCCACACTGGCCTTC 480  
Db 421 CTGGGCAACGACACACTGGGCCCTCTGAGTCTCTCCAGTGTGCTGCCACACTGGCCTTC 480  
Qy 481 TCCACACGAGTACATCAATGGCCAGATGATCTGTTATGACATGACGACGACGAGAAAT 540  
Db 481 TCCACACGAGTACATCAATGGCCAGATGATCTGTTATGACATGACGACGACGAGAAAT 540  
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 600  
Db 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 600  
Qy 601 GGTCAATTTGTGTGCTATTACATGATGGTCAGAGCCTGATCAAGCCAGGAGAACCT 660  
Db 601 GGTCAATTTGTGTGCTATTACATGATGGTCAGAGCCTGATCAAGCCAGGAGAACCT 660  
Qy 661 CATGAGACAGGCAACACAGCCGAGCCAGTCCATCGGACCATCTACTGTTGTGTGG 720  
Db 661 CATGAGACAGGCAACACAGCCGAGCCAGTCCATCGGACCATCTACTGTTGTGTGG 720  
Qy 721 CCTCTTCAACCTCTGTTTGTGCGCTTCCATATCACTCGCTCTCTTACCTCACCATTG 780  
Db 721 CCTCTTCAACCTCTGTTTGTGCGCTTCCATATCACTCGCTCTCTTACCTCACCATTG 780  
Qy 781 CTTCCTGCTTCTCAGAGTGCAGCTCTTGATGGGAGCCAGTGTGGCTTACAGATATG 840  
Db 781 CTTCCTGCTTCTCAGAGTGCAGCTCTTGATGGGAGCCAGTGTGGCTTACAGATATG 840  
Qy 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGGGG 900  
Db 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGGGG 900

Db 841 GAGGCTCTGCTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGGGG 900  
Qy 901 GGCAAAAATAGAGTCAAGGCTCTCTCCAGAAACTGAGGAGAAACAAGTTGGTGAGCATCCA 960  
Db 901 GGCAAAAATAGAGTCAAGGCTCTCTCCAGAAACTGAGGAGAAACAAGTTGGTGAGCATCCA 960  
Qy 961 GCTGGGAGGAGAGATGCCCGAGGTTTGAACAGATCTGGGTAA 1002  
Db 961 GCTGGGAGGAGAGATGCCCGAGGTTTGAACAGATCTGGGTAA 1002  
RESULT 2  
ADB99267  
ID ADB99267 standard; cDNA; 1156 BP.  
XX  
AC ADB99267;  
XX AC  
DT 04-DEC-2003 (first entry)  
XX Human p2Y2li cDNA.  
XX  
KW ss; gene; human; P2Y2li; chromosome 3; G protein-coupled receptor; GPCR;  
KW Class A rhodopsin-like sub-family; gene therapy.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
CDS 21..1106  
FT /\*tag= a  
FT /product= "P2Y2li"  
XX  
PN DE10144044-A1.  
XX  
PD 27-MAR-2003.  
XX  
PF 07-SEP-2001; 2001DE-01044044.  
XX  
PR 07-SEP-2001; 2001DE-01044044.  
XX  
PA (BRUE/) BRUESS M.  
PA (BOEN/) BOENISCH H.  
PA (VKUE/) VON KUEGELGEN I.  
XX  
PI Bruess M, Boenisch H, Von Kuegelgen I;  
XX  
DR WPI; 2003-364675/35.  
DR P-PSDB; ADB99264.  
XX  
PT New human gene P2Y2li and encoded G protein-coupled receptor, useful for  
PT treatment and diagnosis of receptor-associated diseases and for drug  
PT screening.  
XX  
PS Disclosure; Page 4; 6pp; German.  
XX  
CC This invention describes the human P2Y2li gene and its 5'- and 3'-  
CC untranslated regions, located on chromosome 3 which is a novel G protein-  
CC coupled receptor (GPCR). The protein encoded by P2Y2li is expressed in  
CC blood cells, testis and embryonal kidney cells and contains potential  
CC sites for phosphorylation by protein kinase C and casein kinase II. It is  
CC a member of the Class A rhodopsin-like sub-family of G protein-coupled  
CC receptors and it probably a nucleoside/nucleotide receptor that mediates  
CC action of nucleosides/nucleotides or their sugar derivatives. P2Y2li and  
CC antibodies directed against the encoded protein are useful in diagnosis  
CC and treatment (including gene therapy) of diseases associated with  
CC abnormal levels of P2Y2li expression, in screening assays for modulators,  
CC potential therapeutic agents, and to produce transgenic animals, e.g. for  
CC identifying diseases associated with abnormal expression of P2Y2li. This  
CC sequence represents the P2Y2li gene described in the disclosure of the  
CC invention.  
XX  
SQ Sequence 1156 BP; 243 A; 335 C; 295 G; 283 T; 0 U; 0 Other;  
Query Match 99.8%; Score 1000.4; DB 10; Length 1156;

Best Local Similarity 99.9%; Pred. No. 2.2e-262;		Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	ATGAGAAAGGTGGACATGAATACATCACAGGAAACAAGGTCCTCTGCGCAGTTTCTCAGAGAAG	60
Db	105	ATGAGAAAGGTGGACATGAATACATCACAGGAAACAAGGTCCTCTGCGCAGTTTCTCAGAGAAG	164
Qy	61	TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTCTAGGGCTGCCACTA	120
Db	165	TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTCTAGGGCTGCCACTA	224
Qy	121	AATGGCACTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC	180
Db	225	AATGGCACTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC	284
Qy	181	TATCTGCTGAACCTGATGTGGCCGCACTCTGCTTTATGTGCTATTGCGCCTTCCTCATCATC	240
Db	285	TATCTGCTGAACCTGATGTGGCCGCACTCTGCTTTATGTGCTATTGCGCCTTCCTCATCATC	344
Qy	241	ACCTACTCATAGATGACAGGTGGCCCTTCGGGGAGTGTCTGTGCAAGCTGGTGCACTTC	300
Db	345	ACCTACTCATAGATGACAGGTGGCCCTTCGGGGAGTGTCTGTGCAAGCTGGTGCACTTC	404
Qy	301	CTGTTCTATCAACTTACAGCAGCATCCTGCTGCTGACCTGCACTCTGTGCAACAG	360
Db	405	CTGTTCTATCAACTTACAGCAGCATCCTGCTGCTGACCTGCACTCTGTGCAACAG	464
Qy	361	TTCTTAGTGTGTGCCACCACTGTGTTGCTGCCCCTACCGGACCCCGACGGCATGCGCTGG	420
Db	465	TTCTTAGTGTGTGCCACCACTGTGTTGCTGCCCCTACCGGACCCCGACGGCATGCGCTGG	524
Qy	421	CTGGGCACAGCACACAGCTGGGCCCTCGGTGGTCTCTCAGCTGTGTCGCCACACTGGGCCCTC	480
Db	525	CTGGGCACAGCACACAGCTGGGCCCTCGGTGGTCTCTCAGCTGTGTCGCCACACTGGGCCCTC	584
Qy	481	TCCACACGACATACATCAATGCGCAGATCATCTGTGTATGACATGACACGCCAAGAGAAT	540
Db	585	TCCACACGACATACATCAATGCGCAGATCATCTGTGTATGACATGACACGCCAAGAGAAT	644
Qy	541	TTTGATCGGCTTTTGTGCTACGGCATAGTTCTGACATTTGTCTGGCTTTCTTCCCTCCTT	600
Db	645	TTTGATCGGCTTTTGTGCTACGGCATAGTTCTGACATTTGTCTGGCTTTCTTCCCTCCTT	704
Qy	601	GGTCATTTTGGTGTGCTATTCACTGATGTGTGAGAGGCTGATCAAGCCAGAGAGAACCT	660
Db	705	GGTCATTTTGGTGTGCTATTCACTGATGTGTGAGAGGCTGATCAAGCCAGAGAGAACCT	764
Qy	661	CATGAGCAGGCAACACAGCCGAGCCAGGTCATCCGGACCATCTACTGTGTGTGG	720
Db	765	CATGAGCAGGCAACACAGCCGAGCCAGGTCATCCGGACCATCTACTGTGTGTGG	824
Qy	721	CCTCTTCCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCCTTCTACCTCACCATCTG	780
Db	825	CCTCTTCCACCTCTGTTTGTGGCCCTTCCATATCACTCGCTCCTTCTACCTCACCATCTG	884
Qy	781	CTTCTGCTTTCTCAGAGTCGCAAGCTCTTTGATGGCAGCCAGTGTGGCTTACAAGATATG	840
Db	885	CTTCTGCTTTCTCAGAGTCGCAAGCTCTTTGATGGCAGCCAGTGTGGCTTACAAGATATG	944
Qy	841	GAGGCTCTGGTCAGTGTGAGCAGCTGCTCAACCCAGTCTGCTACTTTCTTTCAAGGGG	900
Db	945	GAGGCTCTGGTCAGTGTGAGCAGCTGCTCAACCCAGTCTGCTACTTTCTTTCAAGGGG	1004
Qy	901	GGCAAAATAGAGTCAGGCTCTCTCCAGAAACTGAGGCAGAAACAAGTTGGGTGAGCATCCA	960
Db	1005	GGCAAAATAGAGTCAGGCTCTCTCCAGAAACTGAGGCAGAAACAAGTTGGGTGAGCATCCA	1064
Qy	961	GCTGGGAGGAAGAGATGCCCGAGGTTGAAACAGATCTGGGTAA	1002
Db	1065	GCTGGGAGGAAGAGATGCCCGAGGTTGAAACAGATCTGGGTAA	1106

### RESULT 3

ADCB6166	ADCB6166 standard; DNA; 1334 BP.
XX	AC
XX	AC
XX	AC
XX	AC
DT	01-JAN-2004 (first entry)
XX	Human GPCR gene SEQ ID NO:619.
XX	ds; gene; human; GPCR;
XX	guanosine triphosphate-binding protein coupled receptor; gene therapy.
XX	Homo sapiens.
XX	BP1270724-A2.
XX	02-JAN-2003.
XX	18-JUN-2002; 2002EP-00013517.
XX	18-JUN-2001; 2001JP-00246789.
XX	(NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX	(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
XX	Suwa M, Asai K, Akiyama Y, Aburatani H;
XX	WPI; 2003-315783/31.
XX	P-PSDB; ADCB6167.
XX	New polynucleotide, useful for preparing a composition for treating a
XX	patient in need of increased or suppressed activity or expression of the
XX	guanosine triphosphate-binding protein coupled receptor.
XX	Claim 1; SEQ ID NO 619; 28pp; English.
XX	The invention relates to a novel polynucleotide encoding a guanosine
XX	triphosphate-binding protein coupled receptor (GPCR). A polynucleotide of
XX	the invention may have a use in gene therapy. The polynucleotide and
XX	polypeptide are useful for preparing a composition for treating a patient
XX	in need of increased or suppressed activity or expression of the
XX	guanosine triphosphate-binding protein coupled receptor. The
XX	polynucleotide sequences shown in ADCB5548-ADCB7616 encode GPCR's of the
XX	invention.
XX	Sequence 1334 BP; 283 A; 368 C; 348 G; 335 T; 0 U; 0 Other;
QY	Query Match 99.8%; Score 1000.4; DB 10; Length 1334;
Db	Best Local Similarity 99.9%; Pred. No. 2.3e-262;
QY	Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	1 ATGAGAGGTGACATGAATACATACACAGGACAAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db	201 ATGAGAGGTGACATGAATACATACACAGGACAAAGGTCTCTGCCAGTTCTCAGAGAAG 260
QY	61 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db	261 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 320
QY	121 AATGGCACTCTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180
Db	321 AATGGCACTCTCTTGTGGCACTCTGGGGCCAAACCAAGCGCTGTGCCACCACC 380
QY	181 TATCTGGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTATTGCGCTTCTCATCATC 240
Db	381 TATCTGGTGAACCTGATGGTGGCCGACCTGCTTTATGTGCTATTGCGCTTCTCATCATC 440
QY	241 ACCTACTCACTAGATGACAGTGGCCCTCTCGGGGAGCTGCCTCTGCAAGCTGGTGCATTC 300
Db	441 ACCTACTCACTAGATGACAGTGGCCCTCTCGGGGAGCTGCCTCTGCAAGCTGGTGCATTC 500
QY	301 CTGTTCTTATATCAACCTTTATCGGCAGCATCCTGCTGTGTGACCTGATCTCTGTGCCAG 360

Db 501 CTGTTCTATATCAACCTTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACAG 560  
Qy 361 TTCCTAGGTGTGCCACCCACTGTGTTGCTGCTGCCCTACCGGACCCCGAGGCATGCTCTGG 420  
Db 561 TTCCTAGGTGTGCCACCCACTGTGTTGCTGCTGCCCTACCGGACCCCGAGGCATGCTCTGG 620  
Qy 421 CTGGGCACACGACCACTGGGCGCTGGTGTCTCTCCAGCTGTGCTCCACCACTGGCCTTC 480  
Db 621 CTGGGCACACGACCACTGGGCGCTGGTGTCTCTCCAGCTGTGCTCCACCACTGGCCTTC 680  
Qy 481 TCCACACGGAATACATCAATGGGCGAGATGCTGTGTATGATGACGACGACCAAGAGAT 540  
Db 681 TCCACACGGAATACATCAATGGGCGAGATGCTGTGTATGATGACGACGACCAAGAGAT 740  
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 600  
Db 741 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTCTTTCCCTCCTT 800  
Qy 601 GGTCAATTTGTGTGCTATTCACTGATGGTCAGGAGCTGATCAAGCAGGAGAACCT 660  
Db 801 GGTCAATTTGTGTGCTATTCACTGATGGTCAGGAGCTGATCAAGCAGGAGAACCT 860  
Qy 661 CATGAGCAGGCAACACAGCCGAGCCAGTCCATCCGACCATCTCTACTGTGTGTGG 720  
Db 861 CATGAGCAGGCAACACAGCCGAGCCAGTCCATCCGACCATCTCTACTGTGTGTGG 920  
Qy 721 CCTTTACACCTCTGTTTTGTGCGCTTCCATPACATCGCTCTCTTACCTCACCACCTG 780  
Db 921 CCTCTTACCTCTGTTTTGTGCGCTTCCATPACATCGCTCTCTTACCTCACCACCTG 980  
Qy 781 CTTTCTGCTTCTCAGACTGCCAGCTCTTGATGGCAGCAGTGTGCTTACAGATATG 840  
Db 981 CTTTCTGCTTCTCAGACTGCCAGCTCTTGATGGCAGCAGTGTGCTTACAGATATG 1040  
Qy 841 GAGCCTCTGCTGAGTGTGACAGCTGCTCAACCCAGTCTCTGACTTTCTTTCAAGGGG 900  
Db 1041 GAGCCTCTGCTGAGTGTGACAGCTGCTCAACCCAGTCTCTGACTTTCTTTCAAGGGG 1100  
Qy 901 GGCAAAATAGAGTCAGGCTCTCTCAGAAATCTGAGGAGCAACAGTTGGGTGAGCATCCA 960  
Db 1101 GGCAAAATAGAGTCAGGCTCTCTCAGAAATCTGAGGAGCAACAGTTGGGTGAGCATCCA 1160  
Qy 961 GCTGGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1002  
Db 1161 GCTGGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1202

RESULT 4

AAS17746  
ID AAS17746 standard; DNA; 3143 BP.

XX AC AAS17746;  
XX AC  
XX DT 26-FEB-2002 (first entry)  
XX DE Human genomic clone for P2Y-like G protein-coupled receptor.  
XX KW Human; ds; P2Y-like G protein-coupled receptor; GPCR; COPD;  
KW chronic obstructive pulmonary disease; nervous system disease;  
KW Parkinson's disease; multiple sclerosis; dementia; stroke;  
KW Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;  
KW bacterial infection; fungal infection; protozoan infection;  
KW viral infection; pain; cancer; anorexia; bulimia; asthma;  
KW acute heart failure; hypertension; hypertensive; osteoporosis; diabetes;  
KW angina pectoris; myocardial infarction; ulcer; inflammation; allergy;  
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
KW manic depression; delirium; severe mental retardation; dyskinesia.  
XX OS Homo sapiens.  
XX PH  
XX FT Key Location/Qualifiers  
XX CDS 520..2498  
FT /\*tag= a

FT XX /product= "P2Y-like GPCR"  
XX PN WO200185764-A2.  
XX PD 15-NOV-2001.  
XX PF 09-MAY-2001; 2001WO-EP005244.  
XX PR 11-MAY-2000; 2000US-0203582P.  
XX PR 21-FEB-2001; 2001US-0269857P.  
XX PA (FARB ) BAYER AG.  
XX PI Ramakrishnan S;  
XX DR WPI; 2002-075242/10.  
XX DR P-PSDB; AAU11251.  
XX FT New polynucleotides for producing P2Y-like G protein-coupled receptors  
FT (GPCR) that are used for screening inhibitors or regulators of human P2Y-  
FT like GPCR, especially useful for treating pain, cancer or neurological  
FT disorders.  
XX PS Disclosure; Fig 1; 114pp; English.  
XX CC The invention relates to an isolated polynucleotide encoding a P2Y-like G  
CC protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or  
CC allele, a host cell containing an expression vector comprising the  
CC polynucleotide and screening for agents that regulate the GPCR activity.  
CC The polynucleotide is useful for producing P2Y-like GPCR polypeptide,  
CC which may be employed for screening agents that inhibit or regulate human  
CC P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is  
CC useful for treating or ameliorating P2Y-like GPCR disorders, particularly  
CC COPD (chronic obstructive pulmonary disease), peripheral or central  
CC nervous system disease (e.g. Parkinson's disease, multiple sclerosis,  
CC dementia, stroke, Alzheimer's disease and many other diseases and  
CC disorders listed in the specification), benign prostatic hyperplasia or  
CC urinary incontinence. A pharmaceutical composition containing the  
CC modulators and/or regulators of P2Y-like GPCR is useful for modulating  
CC the activity of a P2Y-like GPCR. In particular, these are useful for  
CC treating, preventing or ameliorating infections (e.g. bacterial, fungal,  
CC protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,  
CC acute heart failure, hypertension, hypertensive, osteoporosis, diabetes,  
CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,  
CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic  
CC depression, delirium, severe mental retardation or dyskinesias). The  
CC present sequence is a genomic clone encoding the P2Y-like GPCR of the  
CC invention  
XX SQ Sequence 3143 BP; 818 A; 771 C; 726 G; 828 T; 0 U; 0 Other;  
Query Match 99.8%; Score 1000.4; DB 6; Length 3143;  
Best Local Similarity 99.9%; Pred. No. 3.4e-262;  
Matches 1001; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 ATGGAGAAGGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60  
Db 520 ATGGAGAAGGTGGACATGAATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 579  
Qy 61 TACAGCAAGCTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGCTGCCACTA 120  
Db 580 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGCTGCCACTA 639  
Qy 121 AATGGCACTCTCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 180  
Db 640 AATGGCACTCTCTTTGTGGCACTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACACC 699  
Qy 181 TATCTGGTGAACTCTGATGGTGGCGACCTCTGTTTATGTGCTATTTGCCCTTCTCATCATC 240  
Db 700 TATCTGGTGAACTCTGATGGTGGCGACCTCTGTTTATGTGCTATTTGCCCTTCTCATCATC 759  
Qy 241 ACCTACTCTACATGATGACAGTGGCCCTTCGGGAGCTGCTCTGCAAGCTGGTGCATTC 300





QY 481 TCCACACGAGCTACATCAATGCGCAGATGATCTGGTATGATGACATGACAGCAAGAAAT 540  
DB 565 TCCACACGAGCTACATCAATGCGCAGATGATCTGGTATGATGACATGACAGCAAGAAAT 624  
QY 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTTTCTTTCCCTCCTT 600  
DB 625 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGCTTTTCTTTCCCTCCTT 684  
QY 601 GGTCAATTTGGTGTGCTATTCTCACTGATGGTTCAGAGCCTGATCAAGCCAGAGGAGAACCT 660  
DB 685 GGTCAATTTGGTGTGCTATTCTCACTGATGGTTCAGAGCCTGATCAAGCCAGAGGAGAACCT 744  
QY 661 CATGAGACAGGCAACACAGCCAGCCAGGTCATCGGACCATCTACTGTTGTTGG 720  
DB 745 CATGAGACAGGCAACACAGCCAGCCAGGTCATCGGACCATCTACTGTTGTTGG 804  
QY 721 CCTCTTCACTCTGTTTGTGCTTCCATATCACTCGCTCTTCACTCTCACCATCTG 780  
DB 805 CCTCTTCACTCTGTTTGTGCTTCCATATCACTCGCTCTTCACTCTCACCATCTG 864  
QY 781 CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCGACAGTGTGGCTACAGATATG 840  
DB 865 CTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCGACAGTGTGGCTACAGATATG 924  
QY 841 GAGCCCTCTGGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTCAAGGGG 900  
DB 925 GAGCCCTCTGGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTCAAGGGG 984  
QY 901 GGCAAAATAGAGTCAGCTCCTCAGAACTGAGGAGCAAGATTTGGGTGAGCATCCA 960  
DB 985 GGCAAAATAGAGTCAGCTCCTCAGAACTGAGGAGCAAGATTTGGGTGAGCATCCA 1044  
QY 961 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTGG 998  
DB 1045 GCTGGGAGGAGAGATGCCAGGGTTGAACAGATCTGG 1082  
  
RESULT 6  
AAS98135  
ID AAS98135 standard; DNA; 1063 BP.  
AC AAS98135;  
XX  
DT 12-MAR-2002 (first entry)  
XX  
DE Human DNA for potential G protein-coupled receptor #92.  
XX  
KW Human; G protein-coupled receptor; GPCR; ds; GAL4; galanin receptor;  
KW Alzheimer's disease; ankyrotrophic lateral sclerosis; asthma;  
KW atherosclerosis; basal cell carcinoma; breast carcinoma; cardiomyopathy;  
KW chondrosarcoma; chronic obstructive pulmonary disease; Crohn's disease;  
KW depression; epilepsy; macular degeneration; lymphoma; melanoma;  
KW multiple sclerosis; osteoarthritis; osteoporosis; Parkinson's disease;  
KW psoriasis; rheumatoid arthritis; schizophrenia; ulcerative colitis;  
KW tuberculosis; cognition disorder; memory disorder; anorexia;  
KW hormonal release disorder; cardiovascular activity disorder;  
KW pain perception disorder; obesity; diabetes; diabetes; diabetes;  
KW hyperlipidaemia; stroke; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200185791-A1.  
XX  
XX  
PD 15-NOV-2001.  
XX  
PF 11-MAY-2001; 2001WO-US015332.  
XX  
PR 11-MAY-2000; 2000US-0203217P.  
PR 18-MAY-2000; 2000US-0205945P.  
XX  
PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
XX

PI Brown JP, Miller M, Burmer G, Fabre-Suver C, Pritchard D;  
XX WPI; 2002-066595/09.  
DR  
XX  
PT Novel G protein-coupled receptor polypeptides including galanin receptor  
PT polypeptides useful for identifying modulators that are useful for  
PT treating Alzheimer's disease, psoriasis, melanoma, multiple sclerosis,  
PT stroke.  
XX  
PS Claim 2; Page 98; 144pp; English.  
XX  
CC The invention relates to an isolated polypeptide encoded by a nucleic  
CC acid molecule that is at least 80% identical to the G protein-coupled  
CC (GPCR) polynucleotides included in the specification. Also included are  
CC probes based on the GPCR sequences (including antisense probes), a host  
CC cell comprising an expression vector comprising the GPCR sequence,  
CC antibodies raised against the polypeptides, and methods of identifying  
CC modulators of the polypeptides. The polypeptides are useful for  
CC identifying modulator compounds which function as modulators, activators,  
CC repressors, agonists or antagonists of the novel GPCR polypeptides  
CC including the GAL4 polypeptide. The antibodies and nucleic acid probes as  
CC described above can be used to detect the presence of the polypeptides  
CC and nucleic acids and are used to diagnose a variety of diseases or  
CC disorders in which GPCRs are involved e.g. Alzheimer's disease,  
CC ankyrotrophic lateral sclerosis, asthma, atherosclerosis, basal cell  
CC carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic  
CC obstructive pulmonary disease, Crohn's disease, depression, epilepsy,  
CC macular degeneration, lymphoma, melanoma, multiple sclerosis,  
CC osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid  
CC arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other  
CC diseases listed in the specification. The probes and antibodies are also  
CC useful for diagnosing cognition and memory disorders, pain perception  
CC release disorders, cardiovascular activity disorders, pain perception  
CC disorders, obesity, diabetes, Alzheimer's disease. Preferably, compounds  
CC that decrease or increase the expression of galanin receptor (GAL4) can  
CC be used to treat obesity, diabetes, hyperlipidaemia and stroke. The GPCR  
CC nucleic acid is useful for treating the above mentioned disorders by gene  
CC therapy techniques. The present sequence is a novel GPCR polynucleotide  
CC of the invention  
XX  
SQ Sequence 1063 BP; 216 A; 315 C; 272 G; 260 T; 0 U; 0 Other;  
  
Query Match 98.1%; Score 983.4; DB 6; Length 1063;  
Best Local Similarity 99.8%; Pred. No. 9.1e-258;  
Matches 995; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
  
QY 1 ATGGAGAAGTGGACATGAATACATACACAGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 60  
DB 67 ATGGAGAAGTGGACATGAATACATACACAGAAACAGGTCTCTGCCAGTTCTCAGAGAAG 126  
QY 61 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120  
DB 127 TACAAGCAAGTCTACCTCTCCCTGGCCCTACAGTATCATCTTTATCTAGGGCTGCCACTA 186  
QY 121 AATGGCACTCTCTGTGGCACTCTTGGGGCCCAACCAAGCGCTGGCCACCACC 180  
DB 187 AATGGCACTCTCTGTGGCACTCTTGGGGCCCAACCAAGCGCTGGCCACCACC 246  
QY 181 TATCTGGTGAACCTGTATGGTGGCCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 240  
DB 247 TATCTGGTGAACCTGTATGGTGGCCGACCTGCTTTATGTGCTATTGCCCTTCTCATCATC 306  
QY 241 ACCTACTCACTAGATGACAGGTGGCCCTTGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300  
DB 307 ACCTACTCACTAGATGACAGGTGGCCCTTGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 366  
QY 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTACCTCATCTCTGTGCACCA 360  
DB 367 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGTGCTGACCTGCTCTGTGCACCA 426  
QY 361 TTCCTAGGTGTGTGCCACCCCACTGTGTGCTGCTCCCTACCGGACCCCGAGCATGCTCTGG 420  
DB 427 TTCCTAGGTGTGTGCCACCCCACTGTGTGCTGCTCCCTACCGGACCCCGAGCATGCTCTGG 486



PT New NOVX polypeptides and nucleic acids, useful for preventing or  
PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
PT pharmacogenomics.

XX Claim 8; SEQ ID NO 165; 1498pp; English.

XX  
CC This invention relates to a novel nucleic acids, and encoded polypeptides  
CC thereof, which have properties related to the stimulation of biochemical  
CC or physiological responses in a cell, tissue, organ or organism.  
CC Specifically, it refers to the use of biologically active fragments for  
CC diagnostic and prognostic assays and furthermore in the treatment of  
CC diverse pathological conditions. The present invention describes novel  
CC human and murine NOVX proteins, as well as methods to modulate their  
CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
CC The NOVX polypeptides, polynucleotides and antibodies are useful in  
CC treating or preventing NOVX-associated disorders, e.g. cardiomyopathy,  
CC atherosclerosis, cancer and diabetes. Furthermore, they may be used in  
CC treating or preventing diseases such as inflammation, autoimmune  
CC disorders, allergies, blood disorders, acquired immunodeficiency syndrome  
CC (AIDS), obesity, asthma, immunoglobulin (IgA) nephropathy, cirrhosis,  
CC arthritis, Alzheimer's disease, infections, stroke, muscular dystrophy  
CC and epilepsy. Accordingly, these molecules have many activities including  
CC cytosstatic, cardiant, antiinflammatory, immunosuppressive, antiallergic,  
CC haemostatic, anti-HIV, antidiabetic, antiarteriosclerotic, anorectic,  
CC antiaesthetic, nephrotropic, antiarthritic, hepatotropic,  
CC neuroprotective, nootropic, antibacterial, virucide, antiparasitic,  
CC relaxant and anticonvulsant. In addition, they are useful in screening  
CC assays to identify small molecules that modulate or inhibit, for example,  
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
CC used as in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. This polynucleotide is a human NOVX cDNA of the  
CC invention.

XX  
SQ Sequence 1108 BP; 225 A; 321 C; 285 G; 277 T; 0 U; 0 Other;

Query Match 97.58; Score 977.4; DB 6; Length 1108;  
Best Local Similarity 99.74; Pred. No. 4e-256;  
Matches 1000; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
QY 1 ATGAGAGAGGTGGACATGATATACATCACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 60  
DB 96 ATGAGAGAGGTGGACATGATATACATCACAGGAACAAGTCTCTGCCAGTTCTCAGAGAAG 155  
QY 61 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120  
DB 156 TACAAGCAAGTCTACCTCTCCCTGGCCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 215  
QY 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180  
DB 216 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 275  
QY 181 TATCTGTGTGAACCTGTAGTGGCCGACCTGTCTTATGTGTATGTCTATGGCCCTTCTCATCATC 240  
DB 276 TATCTGTGTGAACCTGTAGTGGCCGACCTGTCTTATGTGTATGTCTATGGCCCTTCTCATCATC 335  
QY 241 ACCTACTCTACATAGATGACAGTGGCCCTTGGGGAGCTGTCTGCAAGCTGGTGCATTC 300  
DB 336 ACCTACTCTACATAGATGACAGTGGCCCTTGGGGAGCTGTCTGCAAGCTGGTGCATTC 395  
QY 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAG 360  
DB 396 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAG 455  
QY 361 TTCTAGTGTGTGCCACCCACTGTGTCTGCTGCTGCTACCGGACCCGAGGCATGCTGCG 420  
DB 456 TTCTAGTGTGTGCCACCCACTGTGTCTGCTGCTGCTACCGGACCCGAGGCATGCTGCG 515  
QY 421 CTGGGCAACAGACACCACTGGGCCCTGCTGGTGTCTCCAGCTGTCTGCTGCCACACTGGCCTTC 480  
DB 516 CTGGGCAACAGACACCACTGGGCCCTGCTGGTGTCTCCAGCTGTCTGCTGCCACACTGGCCTTC 575  
QY 481 TCCACACGGACTACATCAATGGCCAGATGATCTGTTATGACATGACCAGCCAGAGAAT 540

DB 576 TCCACACGGACTACATCAATGGCCAGATGATCTGTATGACATGACCAGCCAGAGAAT 635  
QY 541 TTTGATCGGCTTTTGGCTACGCGATAGTTCTGACATTTGTCTGGCTTTCTTTCCCTCCTT 600  
DB 636 TTTGATCGGCTTTTGGCTACGCGATAGTTCTGACATTTGTCTGGCTTTCTTTCCCTCCTT 695  
QY 601 GGTCAATTTGGTGTGTATTTCACTGATGGTTCAGGAGCCTGATCAAGCCAGAGAGAACCT 660  
DB 696 GGTCAATTTGGTGTGT-TATTTCACTGATGGTTCAGGAGCCTGATCAAGCCAGAGAGAACCT 754  
QY 661 CATGAGACAGGCAACAACAGCCCGAGCCAGGTCCATCCGACCATCTACTGTGTGTGG 720  
DB 755 CATGAGACAGGCAACAACAGCCCGAGCCAGGTCCATCCGACCATCTACTGTGTGTGG 814  
QY 721 CCTCTTCAACCTCTGTTTGTGTCCTTCCATATCATCTGCTCCTTCTACCTCACCATCTG 780  
DB 815 CCTCTTCAACCTCTGTTTGTGTCCTTCCATATCATCTGCTCCTTCTACCTCACCATCTG 874  
QY 781 CTTTCTGCTTTCTCAGACTGCGCAGCTCTTGATGGCAG-CCAGTGTGGCCTACAAGATAT 839  
DB 875 CTTTCTGCTTTCTCAGACTGCGCAGCTCTTGATGGCAGCCAGTGTGGCCTACAAGATAT 934  
QY 840 GGAGGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTCTTCAAGGG 899  
DB 935 GGAGGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTACTTTCTTCAAGGG 994  
QY 900 GGCGAAAAATAGAGTACAGGCTCTCCAGAACTCTCAGAGCAACAAGTTGGGTGAGCATCC 959  
DB 995 GGCGAAAAATAGAGTACAGGCTCTCCAGAACTCTCAGAGCAACAAGTTGGGTGAGCATCC 1054  
QY 960 AGCTGGGGAAGAGAGATGCCAGGTTGACAGATCTGGGTAA 1002  
DB 1055 AGCTGGGGAAGAGAGATGCCAGGTTGACAGATCTGGGTAA 1097  
RESULT 8  
ADN42283  
ID ADN42283 standard; cdna; 1108 BP.  
XX  
XX ADN42283;  
XX AC AC  
XX 17-JUN-2004 (first entry)  
XX Human cDNA encoding NOV 43.  
DE  
XX Human; ss; gene; NOVX; cancer; diabetes; cardiomyopathy; atherosclerosis;  
XX SNP; single nucleotide polymorphism.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX variation replace(378,A)  
XX /\*tag= a  
XX /\*standard\_name= "Single nucleotide polymorphism"  
XX variation replace(496,A)  
XX /\*tag= b  
XX /\*standard\_name= "Single nucleotide polymorphism"  
XX US2004033493-A1.  
XX  
XX 19-FEB-2004.  
PD  
XX 31-JAN-2002; 2002US-00072012.  
PF  
XX 31-JAN-2001; 2001US-0265395P.  
PR 31-JAN-2001; 2001US-0265412P.  
PR 31-JAN-2001; 2001US-0265514P.  
PR 31-JAN-2001; 2001US-0265517P.  
PR 02-FEB-2001; 2001US-0266406P.  
PR 05-FEB-2001; 2001US-0266767P.  
PR 07-FEB-2001; 2001US-0266975P.  
PR 07-FEB-2001; 2001US-0267057P.

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PR 08-FEB-2001; 2001US-0267459P.
PR 09-FEB-2001; 2001US-0267823P.
PR 15-FEB-2001; 2001US-0268974P.
PR 26-FEB-2001; 2001US-0271664P.
PR 27-FEB-2001; 2001US-0271839P.
PR 27-FEB-2001; 2001US-0271855P.
PR 02-MAR-2001; 2001US-0272788P.
PR 02-MAR-2001; 2001US-0273046P.
PR 14-MAR-2001; 2001US-0275925P.
PR 14-MAR-2001; 2001US-0275947P.
PR 14-MAR-2001; 2001US-0275950P.
PR 14-MAR-2001; 2001US-0275989P.
PR 15-MAR-2001; 2001US-0276448P.
PR 15-MAR-2001; 2001US-0276450P.
PR 16-MAR-2001; 2001US-0276397P.
PR 16-MAR-2001; 2001US-0276768P.
PR 20-MAR-2001; 2001US-0278652P.
PR 26-MAR-2001; 2001US-0278775P.
PR 26-MAR-2001; 2001US-0278778P.
PR 29-MAR-2001; 2001US-0279882P.
PR 29-MAR-2001; 2001US-0279884P.
PR 30-MAR-2001; 2001US-0280147P.
PR 11-APR-2001; 2001US-0282992P.
PR 11-APR-2001; 2001US-0283083P.
PR 20-APR-2001; 2001US-0285133P.
PR 23-APR-2001; 2001US-0285749P.
PR 03-MAY-2001; 2001US-0288327P.
PR 03-MAY-2001; 2001US-0288504P.
PR 30-MAY-2001; 2001US-0294047P.
PR 30-MAY-2001; 2001US-0294473P.
PR 08-JUN-2001; 2001US-0296964P.
PR 18-JUN-2001; 2001US-0298959P.
PR 19-JUN-2001; 2001US-0299324P.
PR 13-AUG-2001; 2001US-0312020P.
PR 16-AUG-2001; 2001US-0312889P.
PR 16-AUG-2001; 2001US-0312908P.
PR 21-AUG-2001; 2001US-0313930P.
PR 28-AUG-2001; 2001US-0315470P.
PR 31-AUG-2001; 2001US-0316447P.
PR 07-SEP-2001; 2001US-0318115P.
PR 07-SEP-2001; 2001US-0318118P.
PR 12-SEP-2001; 2001US-0318740P.
PR 19-SEP-2001; 2001US-0323379P.
PR 18-OCT-2001; 2001US-0330245P.
PR 18-OCT-2001; 2001US-0330308P.
PR 14-NOV-2001; 2001US-0332701P.
XX
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (SHIM/) SHIMKETS R A.
PA (LILL/) LI L.
PA (GANG/) GANGOLLI E A.
PA (PADI/) PADIGARU M.
PA (ANDE/) ANDERSON D W.
PA (RAST/) RASTELLI L.
PA (MILL/) MILLER C E.
PA (GERL/) GERLACH V.
PA (TAUP/) TAUPIER R J.
PA (GUSE/) GUSEV V Y.
PA (COLM/) COLMAN S D.
PA (WOLE/) WOLENC A R.
PA (PENA/) PENNA C E A.
PA (FURT/) FURTA K.
PA (GROS/) GROSSE W M.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.
PA (BURG/) BURGESS C E.
XX
PI Tchernev VT, Spyttek KA, Zerhusen BD, Patturajan M, Shimkets RA,
PI Li L, Gangolli EA, Padigaru M, Anderson DW, Rastelli L, Miller CE;
PI Gerlach V, Taupier RJ, Gusev VY, Colman SD, Wolenc AR, Pena CEA;
PI Furtak K, Grosse WM, Alsobrook JP, Lepley DM, Rieger DK, Burgess CE;
XX
DR WPI; 2004-180039/17.
DR P-PSDB; ADN42284.
XX
PT Isolated NOVX polypeptides and polynucleotides, useful for preventing
PT diagnosing and/or treating cancer, diabetes, cardiomyopathy and
PT atherosclerosis.
XX
PS Claim 9; SEQ ID NO 165; 1309pp; English.
XX
CC The invention relates isolated 162 NOVX polypeptides (NOV1-NOV99,
CC including splice variants) and the nucleic acids (NA) that encode them.
CC Also included are the mature NOVX proteins (and their encoding
CC polynucleotides), a vector comprising NOVX NA, a cell comprising the
CC vector, an antibody that binds immunospecifically to NOVX, determining
CC the presence or amount of NOVX in a sample, determining the presence or
CC amount of NOVX NA in a sample, identifying an agent that binds to NOVX,
CC modulating the activity of NOVX, treating or preventing a NOVX-associated
CC disorder, determining the presence of or predisposition to a disease
CC associated with altered levels of NOVX and treating a pathological state
CC in a mammal comprising administering a polypeptide which is at least 95%
CC identical to NOVX (or fragment). NOVX and NA may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate expression and activity of NOVX (e.g. cancer, diabetes,
CC cardiomyopathy and/or atherosclerosis). The anti-NOVX antibodies and
CC antagonists may also be used to down regulate expression and activity of
CC NOVX. The anti-NOVX antibodies may also be used as diagnostic agents for
CC detecting the presence of NOVX in samples (e.g. by enzyme linked
CC immunosorbant assay (ELISA). The agents and methods may be used in this
CC way to prevent, diagnose and treat cancer, diabetes, cardiomyopathy
CC and/or atherosclerosis. The present sequence encodes a NOVX protein.
XX
SQ Sequence 1108 BP; 225 A; 321 C; 285 G; 277 T; 0 U; 0 Other;
Query Match 97.5%; Score 977.4; DB 12; Length 1108;
Best Local Similarity 99.7%; Pred. No. 4e-256;
Matches 1000; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy 1 ATGGAGAAGGTGGACATGAATACATACAGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db 96 ATGGAGAAGGTGGACATGAATACATACAGAAACAAGGTCTCTGCCAGTTCTCAGAGAAG 155
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCCTAGGGCTGCCACTA 120
Db 156 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCCTAGGGCTGCCACTA 215
Qy 121 AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACCACC 180
Db 216 AATGGCACTGCTTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCCACCACC 275
Qy 181 TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 240
Db 276 TATCTGGTGAACCTGATGGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 335
Qy 241 ACCTACTACTAGATGACAGGTGGCCCTTCTGGGGAGCTGCTCGCAAGCTGGTGCATTC 300
Db 336 ACCTACTACTAGATGACAGGTGGCCCTTCTGGGGAGCTGCTCGCAAGCTGGTGCATTC 395
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAG 360
Db 396 CTGTTCTATATCAACCTTTACGGCAGCATCTGCTGCTGACCTGCATCTCTGTGCACCAG 455
Qy 361 TTCTTAGGTGTGTCACCCACTGTGTTGCTGTCCTTACCGGACCCCGAGGATGCTCTGG 420
Db 456 TTCTTAGGTGTGTCACCCACTGTGTTGCTGTCCTTACCGGACCCCGAGGATGCTCTGG 515
Qy 421 CTGGGCACACAGCACCCTGGGCCCTTGGTGTCTTCCAGCTGCTGCCACACTGGCCTTC 480
Db 516 CTGGGCACACAGCACCCTGGGCCCTTGGTGTCTTCCAGCTGCTGCCACACTGGCCTTC 575
Qy 481 TCCACACGGGACTACATCAATGGGCAGATGATCTGGTATGACATGACACCGACCAAGAGAAT 540
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Db 576 TCCACACGGACTACATCAATGCGCAGATGATCTGGTATGACATGACACGACCAAGAAAT 635
Qy 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGTGCTTTTCTTCCCTCCTT 600
Db 636 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGTGCTTTTCTTCCCTCCTT 695
Qy 601 GGTCAATTTTGTGTGCTATTCTACATGATGGTCAGAGGCTGATCAAGCCAGAGGAAACCT 660
Db 696 GGTCAATTTTGTGTGCT-TATTCACTGATGGTCAGAGGCTGATCAAGCCAGAGGAAACCT 754
Qy 661 CATGAGACAGGCAACACAGCCAGCCAGGCTCCATCCGACCATCTTACTTGGTGTGTGG 720
Db 755 CATGAGACAGGCAACACAGCCAGCCAGGCTCCATCCGACCATCTTACTTGGTGTGTGG 814
Qy 721 CCTCTTCACCCCTCTGTTTTGTGCGCTTCCATATCACTCGCTTCTTACCTCACCATCTG 780
Db 815 CCTCTTCACCCCTCTGTTTTGTGCGCTTCCATATCACTCGCTTCTTACCTCACCATCTG 874
Qy 781 CTTTCTGTTTCTCAGAGCTGCCAGCTCTTGATGGGAG-CCAGTGTGGCTTACAGATAT 839
Db 875 CTTTCTGTTTCTCAGAGCTGCCAGCTCTTGATGGGAGCCAGTGTGGCTTACAGATAT 934
Qy 840 GGAGCGCTCTGGTCAGTGTGAGAGCTGCCCTCAACCCAGTCTCTACTTTTCAAGGG 899
Db 935 GGAGCGCTCTGGTCAGTGTGAGAGCTGCCCTCAACCCAGTCTCTACTTTTCAAGGG 994
Qy 900 GGGCAAAATAGAGTCAAGGCTCTCCAGAACTGAGGACAGAACTGGGTGAGCATCC 959
Db 995 GGGCAAAATAGAGTCAAGGCTCTCCAGAACTGAGGACAGAACTGGGTGAGCATCC 1054
Qy 960 AGCTGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1002
Db 1055 AGCTGGAGGAGAGATGCCAGGCTTGAACAGATCTGGGTAA 1097

RESULT 9
ADC25999
ID ADC25999 standard; DNA; 1017 BP.
XX
AC ADC25999;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human purinergic receptor P2Y-related GPCR $\alpha$ 6 DNA.
XX
KW virucide; fungicide; antibacterial; cytostatic; analgesic; antidiabetic;
KW anorectic; cardiant; hypotensive; osteopathic; antianginal;
KW antiarteriosclerotic; cerebroprotective; anti-ulcer; antiallergic;
KW nootropic; neuroprotective; antiparkinsonian; G-protein coupled receptor;
KW GPCR; viral; fungal; bacterial infection; immune-related disorder;
KW cancer; pain; diabetes; obesity; anorexia; acute heart failure;
KW hypertension; osteoporosis; angina pectoris; atherosclerosis; stroke;
KW ulcer; allergy; psychotic neurological disorder; schizophrenia; dementia;
KW degenerative disease; Parkinson's; Alzheimer's; dyskinesia; Huntington's;
KW human; GPCR $\alpha$ 6; purinergic receptor P2Y; ds; gene.
XX
OS Homo sapiens.
XX
PH Location/Qualifiers
FT 1..1017
FT /*tag= a
FT /product= "Human purinergic receptor P2Y-related GPCR $\alpha$ 6
FT protein - both "original" and "alternative" versions"
FT /transl_except= (pos:184..186, aa:Pro)
FT /transl_except= (pos:727..729, aa:Xaa)
FT /transl_except= (pos:808..810, aa:Pro)
FT ;note= "Xaa = Unknown; translation exceptions at 184 and
FT 727 are present within "original" protein CDS whilst that
FT at 808 is present within the "alternative" protein CDS"
XX
PN US203088080-A1.
XX
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PD 08-MAY-2003.
XX
PF 21-JUN-2001; 2001US-00885453.
XX
PR 20-JUN-2000; 2000US-0212908P.
PR 05-DEC-2000; 2000EP-00870289.
XX
PA (COMM/) COMMUNI D.
PA (LANIN/) LANNY V.
PA (GOVA/) GOVAERTS C.
PA (PARM/) PARMENTIER M.
PA (DETH/) DETHEUX M.
XX
PI Communi D, Lannoy V, Govaerts C, Parmentier M, Detheux M;
XX
XX WPI; 2003-657983/62.
DR P-PSDB; ADC26000, ADC26009.
XX
XX New human G-protein coupled receptor, useful for treating receptor-
PT mediated disorders, e.g. infections, cancer, pain, diabetes, obesity,
PT acute heart failure, osteoporosis, stroke, ulcer, allergy, or
PT neurological disorders.
XX
XX Example 3; Page 15-16; 24pp; English.
XX
CC The invention relates to a novel G-protein coupled receptor (GPCR). The
CC receptor, polynucleotide, agonist, reverse agonist and antagonist of the
CC invention may be useful for treating receptor-mediated disorders
CC including viral, fungal or bacterial infections, immune-related disorders
CC such as cancer, pain, diabetes, obesity, anorexia, acute heart failure,
CC hypertension, osteoporosis, angina pectoris, atherosclerosis, stroke,
CC ulcer and allergy, as well as psychotic and neurological disorders such
CC as schizophrenia and dementia, degenerative diseases such as Parkinson's
CC disease and Alzheimer's disease and dyskinesias such as Huntington's
CC disease. The current sequence is that of the human purinergic receptor
CC P2Y-related GPCR $\alpha$ 6 DNA of the invention.
XX
SQ Sequence 1017 BP; 200 A; 306 C; 252 G; 259 T; 0 U; 0 Other;
XX
XX Query Match 91.9%; Score 920.4; DB 10; Length 1017;
XX Best Local Similarity 99.8%; Pred. No. 1.4e-240;
XX Matches 932; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Qy 1 ATGGAGAGGTGGACATGATATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60
Db 85 ATGGAGAGGTGGACATGATATACATACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 144
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120
Db 145 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 204
Qy 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACACC 180
Db 205 AATGGCACTGTCTTGTGGCACTTCTGGGGCAACCAAGCGCTGGAGCTGTGCCACACC 264
Qy 181 TATCTGTTGAACCTGATGTGGCGGACCTGCTTTATGTGCTATTCCTTCTCATCATC 240
Db 265 TATCTGTTGAACCTGATGTGGCGGACCTGCTTTATGTGCTATTCCTTCTCATCATC 324
Qy 241 ACCTACTCTACATGATGACAGGTGGCCCTTCGGGGAGCTGCTTGCAGCTGGTGCACTTC 300
Db 325 ACCTACTCTACATGATGACAGGTGGCCCTTCGGGGAGCTGCTTGCAGCTGGTGCACTTC 384
Qy 301 CTGTTCTATATCAACCTTTTACGGCAGCATCCTCTGCTGACCTGCACTCTCTGTGCAACAG 360
Db 385 CTGTTCTATATCAACCTTTTACGGCAGCATCCTCTGCTGACCTGCACTCTCTGTGCAACAG 444
Qy 361 TTCTTAGTGTGTGGCAACCATCTGTTTGGCTGCCCTTACCGGACCCGAGCATGCTGG 420
Db 445 TTCTTAGTGTGTGGCAACCATCTGTTTGGCTGCCCTTACCGGACCCGAGCATGCTGG 504
Qy 421 CTGGGACACAGCACCACTGGGCGCTGGTGGTCTCTCCAGCTGTGCTCCACACTGGCCTTC 480
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Db 864 CTTTCTCTTTCTCAGACGTGCCAGCTCTTGATGGCAGCCAGTGTGCGCTACAAGATATG 923  
Qy 841 GAGGCTCTCTGGTGTGAGTGTGAGCAGTGCCTCAACCCAGTCTCTGTACTTTCTTTCAAGGG 900  
Db 924 GAGGCTCTCTGGTGTGAGTGTGAGCAGTGCCTCAACCCAGTCTCTGTACTTTCTTTCAAGGG 983  
Qy 901 GGC AAAAATAGATCAGGCTCTCCAGAACTGA 934  
Db 984 GGC AAAAATAGATCAGGCTCTCCAGAACTGA 1017

RESULT 11  
ABQ79300  
ID ABQ79300 standard; DNA; 1020 BP.  
XX AC ABQ79300;  
XX 17-OCT-2002 (first entry)  
XX Human GPCR designated PFI-020' encoding sequence.  
XX Human; GPCR; G-protein coupled receptor; antidepressant; neuroleptic;  
KW gene therapy; therapeutic; mood; depression; arousal; eating; sleeping;  
KW disorder; PFI-020'; gene; ds.  
XX Homo sapiens.

OS  
XX  
XX Key Location/Qualifiers  
FH 1..1020  
CDS /\*tag= a  
FT /product= "GPCR designated PFI-020"

XX EPI215214-A1.  
XX 19-JUN-2002.  
XX 04-DEC-2001; 2001EP-00310137.  
XX 18-DEC-2000; 2000GB-00030855.  
PR 17-JAN-2001; 2001GB-00001222.  
XX (PFI2 ) PFIZER LTD.  
XX (PFI2 ) PFIZER INC.  
XX Fidoack MD;  
XX WPI; 2002-510798/55.  
DR P-PSDB; ABB98146.  
XX New polynucleotide encoding G protein-coupled receptor PFI-020, useful  
PT e.g. for treating eating and sleeping disorders and for identifying  
PT specific modulators.  
XX Claim 1 (d); Page 12; 23pp; English.

XX The invention relates to an isolated polynucleotide encoding a novel  
CC polypeptide belonging to the class of proteins known as G-protein coupled  
CC receptors (GPCRs). The activity of proteins of the invention may be  
CC described as, antidepressant and neuroleptic. Polynucleotides of the  
CC invention are used for recombinant expression of the G protein-coupled  
CC receptor (PFI-020) polypeptides, to create transgenic animals, as source  
CC of primers, probes, antisense sequences and ribozymes and in gene  
CC therapy. Therapeutic agents of the invention can be used to treat a wide  
CC range of disorders, particularly mood disorders, depression or arousal,  
CC especially eating and sleeping disorders. The current sequence represents  
CC a coding sequence for a human GPCR designated PFI-020'

XX Sequence 1020 BP; 200 A; 309 C; 252 G; 259 T; 0 U; 0 Other;  
SQ Query Match 91.5%; Score 917.2; DB 6; Length 1020;  
Best Local Similarity 99.5%; Pred. No. 1.1e-239;  
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 ATGAGAAAGGTGACATGATATACATCACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 60  
Db 85 ATGAGAAAGGTGACATGATATACATCACAGGAACAAGGTCTCTGCCAGTTCTCAGAGAAG 144  
Qy 61 TACAAGCAAGTCTACCTCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120  
Db 145 TACAAGCAAGTCTACCTCTCTCCCTGGGCTACAGTATCATCTTTATCTTAGGGCTGCCACTA 204  
Qy 121 AATGGCACTGTCTGTGGGCACTCTTGGGGCAAAACCAAGGGCTGGAGCTGTGCCACACC 180  
Db 205 AATGGCACTGTCTGTGGGCACTCTTGGGGCAAAACCAAGGGCTGGAGCTGTGCCACACC 264  
Qy 181 TATCTGGTGAACCTGTATGGTGGCGGACCTGCTTTATGTGCTATTGGCCCTTCTCATCATC 240  
Db 265 TATCTGGTGAACCTGTATGGTGGCGGACCTGCTTTATGTGCTATTGGCCCTTCTCATCATC 324  
Qy 241 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300  
Db 325 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGGAGCTGCTCTGCAAGCTGGTGCACTTC 384  
Qy 301 CTCTTCTATATCAACCTTTACGGCAGCATCTCTGCTGACCTGCACTCTGTGCAACAG 360  
Db 385 CTCTTCTATATCAACCTTTACGGCAGCATCTCTGCTGACCTGCACTCTGTGCAACAG 444  
Qy 361 TTCTTAGGTGTGTGCCACCCACTGTGTGGTGGCTTACCGGACCCGCGAGCATGCTCTGG 420  
Db 445 TTCTTAGGTGTGTGCCACCCACTGTGTGGTGGCTTACCGGACCCGCGAGCATGCTCTGG 504  
Qy 421 CTGGGCAACAGCAGCACCCTGGGCTTGGTGGCTCTCAGCTGCTGCCACACACTGGCCCTTC 480  
Db 505 CTGGGCAACAGCAGCACCCTGGGCTTGGTGGCTCTCAGCTGCTGCCACACACTGGCCCTTC 564  
Qy 481 TCCCAACGGACTACATCAATAGGCCAGATGATCTGTGTATGACATGACACAGCAAGAAT 540  
Db 565 TCCCAACGGACTACATCAATAGGCCAGATGATCTGTGTATGACATGACACAGCAAGAAT 624  
Qy 541 TTTGATCGGCTTTTGGCTACGGCAGTAGTTCTGACATTTGCTGGCTTTCTTTT--CCCTCC 598  
Db 625 TTTGATCGGCTTTTGGCTACGGCAGTAGTTCTGACATTTGCTGGCTTTCTTTCCCTCC 684  
Qy 599 TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAAGGAGCTGATCAAGCCAGAGGAGAAC 658  
Db 685 TTGGTCAATTTTGGTGTGCTATTCACTGATGGTCAAGGAGCTGATCAAGCCAGAGGAGAAC 744  
Qy 659 CTATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACCAATCTTACTGGTGTGT 718  
Db 745 CTATGAGGACAGGCAACACAGCCCGAGCCAGGTCCATCCGGACCAATCTTACTGGTGTGT 804  
Qy 719 GGCCTCTTACCCCTCTGTTTGTGGCTTCCATATCACTCGCTCTTCTACCTCACCATC 778  
Db 805 GGCCTCTTACCCCTCTGTTTGTGGCTTCCATATCACTCGCTCTTCTACCTCACCATC 864  
Qy 779 TGCTTTCTGCTTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA 838  
Db 865 TGCTTTCTGCTTTTCTCAGGACTGCCAGCTCTTGATGGCAGCCAGTGTGGCTTACAAGATA 924  
Qy 839 TGGAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTATCTTTCTTTCAAG 898  
Db 925 TGGAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTCTGTATCTTTCTTTCAAG 984  
Qy 899 GGGGCAAAAATAGAGTCAAGCTCTCTCCAGAACTGA 934  
Db 985 GGGGCAAAAATAGAGTCAAGCTCTCTCCAGAACTGA 1020

RESULT 12  
AAD29667  
ID AAD29667 standard; cDNA; 1076 BP.  
XX  
XX AAD29667;  
XX  
XX AAD29667;  
DT 17-MAY-2002 (first entry)  
XX



Human G-protein coupled receptor (GCRC-1) cDNA.

Human; G-protein coupled receptor; GCRC-1; cell proliferative disorder; neurological; cardiovascular; gastrointestinal; autoimmune; inflammatory; metabolic; hepatitis; psoriasis; cancer; epilepsy; Alzheimer's disease; Pick's disease; Huntington's disease; Parkinson's disease; hypertension; atherosclerosis; myocardial infarction; gastritis; cirrhosis; cytostatic; osteoporosis; Crohn's disease; acquired immunodeficiency syndrome; AIDS; anaemia; asthma; rheumatoid arthritis; diabetes; obesity; drug screening; transgenic animal; allergy; gene therapy; hepatotropic; anticonvulsant; neurotropic; neuroprotective; cardiac; immunosuppressive; anorectic; virucide; gene; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 57..1076  
/\*tag= a

/product= "Human GCRC-1"

W0200210387-A2.

07-FEB-2002.

25-JUL-2001; 2001WO-US023433.

27-JUL-2000; 2000US-0221478P.

03-AUG-2000; 2000US-0223268P.

21-AUG-2000; 2000US-0227054P.

08-SEP-2000; 2000US-0231121P.

13-SEP-2000; 2000US-0232243P.

15-SEP-2000; 2000US-0232691P.

22-SEP-2000; 2000US-0235146P.

(INCY-) INCYTE GENOMICS INC.

Thornton M, Patterson C, Lal P, Burford N, Yue H, Gandhi AR;  
Elliot VS, Ramkumar J, Baughn MR, Kallick DA, Walia NK, Hafalia AJA;  
Yao MG, Lu Y, Tribouley CM, Policky JL, Kearney L, Gaul RC;  
Warren BA, Lee AE, Ding L;

WPI; 2002-188744/24.

P-PSDB; NAE18640.

New human G-protein coupled receptor polypeptide for diagnosis, prevention and treatment of cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory, and metabolic disorders.

Claim 5; Page 137-138; 150pp; English.

The invention relates to novel human G-protein coupled receptors (GCRC) and their encoding polynucleotides. GCRC is useful as an immunogen for preparing monoclonal and polyclonal antibodies. GCRC is useful for diagnosing, treating and preventing a cell proliferative disorder (e.g., hepatitis, psoriasis, cancer), a neurological disorder (e.g., epilepsy, Alzheimer's disease, Pick's disease, Huntington's disease, Parkinson's disease), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), gastrointestinal disorder (e.g., gastritis, cirrhosis, Crohn's disease), an autoimmune/inflammatory disorder (e.g., acquired immunodeficiency syndrome (AIDS), allergy, anaemia, asthma, rheumatoid arthritis), a metabolic disorder (e.g., diabetes, obesity, osteoporosis), and viral infections. GCRC is useful in a number of drug screening techniques, and to analyse the proteome of a tissue or cell type. GCRC is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridization probes for mapping naturally occurring genomic sequences. GCRC is useful in Southern or Northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays, and in

CC microarrays utilising fluids or tissues from patients to detect altered  
CC GCRC expression. The present sequence is human GCRC-1 cDNA  
XX  
SQ Sequence 1076 BP; 211 A; 318 C; 274 G; 273 T; 0 U; 0 Other;  
Query Match 91.5%; Score 917.2; DB 6; Length 1076;  
Best Local Similarity 99.5%; Pred. No. 1.1e-239;  
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;  
Qy 1 ATGAGAGGTGGACATGATACATACAGGAAAGGTCTCTGCCAGTCTCTCAGAGAG 60  
Db 141 ATGAGAGGTGGACATGATACATACAGGAAAGGTCTCTGCCAGTCTCTCAGAGAG 200  
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGCTGCCACTA 120  
Db 201 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGCTGCCACTA 260  
Qy 121 AATGGCACTGTCTTGTGGCACTCTTGGGGGCAAAACCAAGCGCTGGAGCTGTGCACAC 180  
Db 261 AATGGCACTGTCTTGTGGCACTCTTGGGGGCAAAACCAAGCGCTGTGCACACAC 320  
Qy 181 TATCTGTGTAACCTGATGGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 240  
Db 321 TATCTGTGTAACCTGATGGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 380  
Qy 241 ACCTACTCATTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 300  
Db 381 ACCTACTCATTAGATGACAGGTGGCCCTTCCGGGAGCTGCTCTGCAAGCTGGTGCACTTC 440  
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTCTGACCTGATCTCTGTGACAC 360  
Db 441 CTGTTCTATATCAACCTTTACGGCAGCATCTCTGTCTGACCTGATCTCTGTGACAC 500  
Qy 361 TTCTAGGTGTGGCACCACCTGTTGCTGGTGGCTACCGGACCGGAGCATGCTCTGG 420  
Db 501 TTCTAGGTGTGGCACCACCTGTTGCTGGTGGCTACCGGACCGGAGCATGCTCTGG 560  
Qy 421 CTGGGACACGACACACCTGGGCTCTGGTGGCTCTCAGCTGCTGCCACACTGGCTTC 480  
Db 561 CTGGGACACGACACACCTGGGCTCTGGTGGCTCTCAGCTGCTGCCACACTGGCTTC 620  
Qy 481 TCCACACGGAATACATCAATGGCAGATGATCTGGTATGACATGACACGACCAAGAGAA 540  
Db 621 TCCACACGGAATACATCAATGGCAGATGATCTGGTATGACATGACACGACCAAGAGAA 680  
Qy 541 TTTGATCGCTTTTGGCTACGGCATAGTTCTGACATGCTGGCTTTCTTTT - CCCTCC 598  
Db 681 TTTGATCGCTTTTGGCTACGGCATAGTTCTGACATGCTGGCTTTCTTTTCCCCCTCC 740  
Qy 599 TTGTCATTTTGGTGTGCTATTCACTGATGTCAGGAGCTGATCAAGCCAGAGAGAGAAC 658  
Db 741 TTGTCATTTTGGTGTGCTATTCACTGATGTCAGGAGCTGATCAAGCCAGAGAGAGAAC 800  
Qy 659 CTGATGAGGACAGCAACACAGCCCGAGCCAGGTCCATCCGAGCATCTACTGTGTGT 718  
Db 801 CTGATGAGGACAGCAACACAGCCCGAGCCAGGTCCATCCGAGCATCTACTGTGTGT 860  
Qy 719 GGCTCTTCCACCTCTGTTTGTGGCTTCCATATCACTCGCTCTCTTACTCACCAC 778  
Db 861 GGCTCTTCCACCTCTGTTTGTGGCTTCCATATCACTCGCTCTCTTACTCACCAC 920  
Qy 779 TGTCTTCTGCTTCTCAGGACTGCGAGCTCTTGTATGGCAGCGAGTGTGGCTTACAAGATA 838  
Db 921 TGTCTTCTGCTTCTCAGGACTGCGAGCTCTTGTATGGCAGCGAGTGTGGCTTACAAGATA 980  
Qy 839 TGGAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGG 898  
Db 981 TGGAGGCTCTGTGTGAGTGTGAGCAGCTGCTCAACCCAGTCTGTACTTTCTTTCAAGG 1040  
Qy 899 GGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 934  
Db 1041 GGGGCAAAATAGAGTCAAGCTCTCTCCAGAACTGA 1076

## RESULT 13

AD030395  
XX AD030395 standard; cDNA; 1076 BP.  
XX AC  
XX ADO30395;  
XX  
XX 29-JUL-2004 (first entry)  
XX DE Human GPCR P2Y3L polynucleotide, SEQ ID NO:1498.  
XX KW G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytosatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
KW gene; ss.  
XX OS Homo sapiens.  
XX OS  
XX PN WO2004040000-A2;  
XX  
XX PD 13-MAY-2004.  
XX  
XX PF 09-SEP-2003; 2003WO-US028226.  
XX  
XX PR 09-SEP-2002; 2002US-0409303P.  
XX PR 09-APR-2003; 2003US-0461329P.  
XX  
XX PA (PRIM-) PRIMAL INC.  
XX  
XX PI Galitanarie GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX  
XX WPI; 2004-390329/36.  
XX DR P-PSDB; ADO30394.  
XX  
XX PT Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
XX PS Claim 151; SEQ ID NO 1498; 542pp; English.  
XX  
XX CC The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridise to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,

CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
CC nucleic acid of the invention. Note: The full sequence data for this  
CC patent did not form part of the printed specification; those sequences  
CC not shown were obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 1076 BP; 211 A; 318 C; 274 G; 273 T; 0 U; 0 Other;

Query Match 91.5%; Score 917.2; DB 12; Length 1076;  
Best Local Similarity 99.5%; Pred. No. 1.1e-239;  
Matches 931; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 1 ATGGAGAGGTGGACATGAATATACATACAGAACAGGTCTCTGCCAGTTCTCAGAGAAG 60  
Db 141 ATGGAGAGGTGGACATGAATATACATACAGAACAGGTCTCTGCCAGTTCTCAGAGAAG 200  
Qy 61 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATATCTTTATCTAGGCTGCCACTA 120  
Db 201 TACAAGCAAGTCTACCTCTCCCTGGCTACAGTATATCTTTATCTAGGCTGCCACTA 260  
Qy 121 AATGGCACTCTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 180  
Db 261 AATGGCACTCTCTTGTGGCACTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCACC 320  
Qy 181 TATCTGTGAACCTGATGGTGGCGACCTCTTTATGTGCTATTTGCCCTTCCTCATATC 240  
Db 321 TATCTGTGAACCTGATGGTGGCGACCTCTTTATGTGCTATTTGCCCTTCCTCATATC 380  
Qy 241 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGTCTGCAAGCTGGTGCACTTC 300  
Db 381 ACCTACTCACTAGATGACAGGTGGCCCTTCGGGAGCTGTCTGCAAGCTGGTGCACTTC 440  
Qy 301 CTGTTCTATATCAACCTTTACGGCAGCATCCTGCTGTGACCTGCACTCTGTGCAACAG 360  
Db 441 CTGTTCTATATCAACCTTTACGGCAGCATCCTGCTGTGACCTGCACTCTGTGCAACAG 500  
Qy 361 TTCTTAGGTGTGGCCACCACCTGTGTGGCTGCCCTACCGGACCCGACGCACTGCTGG 420  
Db 501 TTCTTAGGTGTGGCCACCACCTGTGTGGCTGCCCTACCGGACCCGACGCACTGCTGG 560  
Qy 421 CTGGGACCAAGCACCACCTGGGCCCTGGTGGTCTCTCCAGCTGTGCTGCCACACTGGCTTC 480  
Db 561 CTGGGACCAAGCACCACCTGGGCCCTGGTGGTCTCTCCAGCTGTGCTGCCACACTGGCTTC 620  
Qy 481 TCCACACCGGACTACATCAATGGCCAGATGATCTGGTATGACATGACACCGCCAAAGAAAT 540  
Db 621 TCCACACCGGACTACATCAATGGCCAGATGATCTGGTATGACATGACACCGCCAAAGAAAT 680  
Qy 541 TTTGATCGGCTTTTGGCTAGGCAATGTTCTGACATGTTGCTGCTTTCTTTT -CCCTCC 598  
Db 681 TTTGATCGGCTTTTGGCTAGGCAATGTTCTGACATGTTGCTGCTTTCTTTTCCCTCC 740  
Qy 599 TTGCTCATTTTGGTGTGCTATTCACTGATGGTCAAGAGCCTGATCAAGCCAGAGGAGAAC 658  
Db 741 TTGCTCATTTTGGTGTGCTATTCACTGATGGTCAAGAGCCTGATCAAGCCAGAGGAGAAC 800  
Qy 659 CTATAGGAGAGGCAACACAGCCCGAGCAGGTTCATCCGGACCATCTTACTGGTGTGT 718  
Db 801 CTATAGGAGAGGCAACACAGCCCGAGCAGGTTCATCCGGACCATCTTACTGGTGTGT 860  
Qy 719 GGCTCTTTCACCTCTGTTTGTGGCTTCCATATCACTCGCTCTCTTCTACCTCACCATC 778  
Db 861 GGCTCTTTCACCTCTGTTTGTGGCTTCCATATCACTCGCTCTCTTCTACCTCACCATC 920  
Qy 779 TGCTTTCTGCTTTCTCAGGACTGCGAGCTCTTGTATGGCAGCCAGGTGTGGCTTACAAGATA 838  
Db 921 TGCTTTCTGCTTTCTCAGGACTGCGAGCTCTTGTATGGCAGCCAGGTGTGGCTTACAAGATA 980

QY 839 TGGAGGCTCTGGTGAAGTGCAGAGTGCCTCAACCCAGTCTCTACTCTTTTCAAGG 898  
DB 981 TGGAGGCTCTGGTGAAGTGCAGAGTGCCTCAACCCAGTCTCTACTCTTTTCAAGG 1040  
QY 899 GGGGCAAAATAGAGTCAGGCTCTCCAGAACTGA 934  
DB 1041 GGGGCAAAATAGAGTCAGGCTCTCCAGAACTGA 1076

## RESULT 14

AA517747  
ID AAS17747 standard; DNA; 850 BP.

AC AAS17747;

XX 26-FEB-2002 (first entry)

DE Human P2Y-like G protein-coupled receptor exon 1.

XX Human; ds; P2Y-like G protein-coupled receptor; GPCR; COPD;  
KW Chronic obstructive pulmonary disease; nervous system disease;  
KW Parkinson's disease; multiple sclerosis; dementia; stroke;  
KW Alzheimer's disease; benign prostatic hyperplasia; urinary incontinence;  
KW bacterial infection; fungal infection; protozoan infection;  
KW viral infection; pain; cancer; anorexia; bulimia; asthma; exon 1;  
KW acute heart failure; hypotension; hypertension; osteoporosis; diabetes;  
KW angina pectoris; myocardial infarction; ulcer; inflammation; allergy;  
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
KW manic depression; delirium; severe mental retardation; dyskinesia.

XX Homo sapiens.

XX WO200185764-A2.

XX 15-NOV-2001.

XX 09-MAY-2001; 2001WO-EP005244.

PR 11-MAY-2000; 2000US-0203582P.

PR 21-FEB-2001; 2001US-0269857P.

XX (FARB ) BAYER AG.

XX Ramakrishnan S;

XX WPI; 2002-075242/10.

XX New polynucleotides for producing P2Y-like G protein-coupled receptors  
PT (GPCR) that are used for screening inhibitors or regulators of human P2Y-  
PT like GPCR, especially useful for treating pain, cancer or neurological  
PT disorders.

XX Claim 1; Fig 4; 114pp; English.

XX The invention relates to an isolated polynucleotide encoding a P2Y-like G  
CC protein-coupled receptor (GPCR) polypeptide, its fragment, derivative or  
CC allele, a host cell containing an expression vector comprising the  
CC polynucleotide and screening for agents that regulate the GPCR activity.  
CC The polynucleotide is useful for producing P2Y-like GPCR polypeptide,  
CC which may be employed for screening agents that inhibit or regulate human  
CC P2Y-like GPCR. The reagent or inhibitor of the human P2Y-like GPCR is  
CC useful for treating or ameliorating P2Y-like GPCR disorders, particularly  
CC COPD (chronic obstructive pulmonary disease), peripheral or central  
CC nervous system disease (e.g. Parkinson's disease, multiple sclerosis,  
CC dementia, stroke, Alzheimer's disease and many other diseases and  
CC disorders listed in the specification), benign prostatic hyperplasia or  
CC urinary incontinence. A pharmaceutical composition containing the  
CC modulators and/or regulators of P2Y-like GPCR is useful for modulating  
CC the activity of a P2Y-like GPCR. In particular, these are useful for  
CC treating, preventing or ameliorating infections (e.g. bacterial, fungal,  
CC protozoan or viral infections), pain, cancer, anorexia, bulimia, asthma,  
CC acute heart failure, hypotension, hypertension, osteoporosis, diabetes,

CC angina pectoris, myocardial infarction, ulcers, inflammation, allergies,  
CC psychotic or neurological disorders (e.g. anxiety, schizophrenia, manic  
CC depression, delirium, severe mental retardation or dyskinesia). The  
CC present sequence is exon 1 of the P2Y-like GPCR of the invention

XX SQ Sequence 850 BP; 165 A; 262 C; 201 G; 222 T; 0 U; 0 Other;

Query Match 84.7%; Score 848.4; DB 6; Length 850;

Best Local Similarity 99.9%; Pred. No. 5.9e-221;

Matches 849; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAGAAAGTGGACATGAATACATCACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 60

DB 1 ATGGAGAAAGTGGACATGAATACATCACAGAAACAAGTCTCTGCCAGTTCTCAGAGAAG 60

QY 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120

DB 61 TACAAGCAAGTCTACCTCTCCCTGGCTTACAGTATCATCTTTATCTTAGGGCTGCCACTA 120

QY 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 180

DB 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGTGCCACCAACC 180

QY 181 TATCTGTGAACCTGTATGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 240

DB 181 TATCTGTGAACCTGTATGTGGCGACCTGCTTTATGTGCTATTGCTTCTCTCATCATC 240

QY 241 ACCTACTCATTAGATGACAGGTGGCCCTTGGGGAGTGTCTGCGAGCTGGTGCACATTC 300

DB 241 ACCTACTCATTAGATGACAGGTGGCCCTTGGGGAGTGTCTGCGAGCTGGTGCACATTC 300

QY 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGTGCTGTGACCTGCATCTCTGTGCACCAG 360

DB 301 CTGTTCTATATCAACCTTTACGGCAGCATCTGTGCTGTGACCTGCATCTCTGTGCACCAG 360

QY 361 TTCTTAGTGTGTGCCACCACTGTGTTGCTGCTTACCGGACCGGAGCATGCTCTGG 420

DB 361 TTCTTAGTGTGTGCCACCACTGTGTTGCTGCTTACCGGACCGGAGCATGCTCTGG 420

QY 421 CTGGGCAACGACCACTGGGCTTCCAGTGTCTCCAGTGTCTCCACACTGGCCCTTC 480

DB 421 CTGGGCAACGACCACTGGGCTTCCAGTGTCTCCAGTGTCTCCACACTGGCCCTTC 480

QY 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACACGACCAAGAGAT 540

DB 481 TCCACACGGACTACATCAATGGCCAGATGATCTGGTATGACATGACACGACCAAGAGAT 540

QY 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCTT 600

DB 541 TTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTTGCTGGCTTTTCTTCCCTCTT 600

QY 601 GGTCAATTTGGTGTGCTATTTCATGTGCTCAGAGCTGTATCAAGCCAGAGAGAACT 660

DB 601 GGTCAATTTGGTGTGCTATTTCATGTGCTCAGAGCTGTATCAAGCCAGAGAGAACT 660

QY 661 CATCAGACGACGCAACACAGCCGACGCTTCCATCCGACCATCTTACTGCTGTGTGG 720

DB 661 CATCAGACGACGCAACACAGCCGACGCTTCCATCCGACCATCTTACTGCTGTGTGG 720

QY 721 CCTCTTCACTCTGTTTTTGTGGCTTCCATATCATCTGCTCTTCTTACCTCACCATCTG 780

DB 721 CCTCTTCACTCTGTTTTTGTGGCTTCCATATCATCTGCTCTTCTTACCTCACCATCTG 780

QY 781 CTTTCTGCTTTCTCAGAGCTGCCAGTCTTGAATGGCAGCAGTGTGGCTTACAGATATG 840

DB 781 CTTTCTGCTTTCTCAGAGCTGCCAGTCTTGAATGGCAGCAGTGTGGCTTACAGATATG 840

QY 841 GAGGCTCTG 850

DB 841 GAGGCTCTG 850

RESULT 15

AD030397  
ID ADO30397 standard; cDNA; 906 BP.  
XX  
AC ADO30397;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Mouse GPCR P2Y3L polynucleotide, SEQ ID NO:1500.  
XX  
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cytosatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
KW murine; gene; ss.  
XX  
OS Mus musculus.  
XX  
XX WO2004040000-A2.  
XX  
XX 13-MAY-2004.  
XX  
XX 09-SEP-2003; 2003WO-US028226.  
XX  
XX 09-SEP-2002; 2002US-0409303P.  
XX  
XX 09-APR-2003; 2003US-0461329P.  
XX  
XX (PRIM-) PRIMAL INC.  
XX  
XX Gitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX  
XX WPI; 2004-390329/36.  
XX  
XX P-PSDB; ADO30396.  
XX  
XX Novel mammalian G protein coupled receptors, useful for identifying  
PT compounds that modulates diagnosing and treating disease condition  
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
PT pectoris, Parkinson's disease.  
XX  
XX Claim 151; SEQ ID NO 1500; 542pp; English.  
XX  
XX The invention relates to human and mouse G protein-coupled receptors  
CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
CC of the invention; methods of treating, preventing or diagnosing diseases  
CC associated with GPCRs of the invention; methods of screening for  
CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
CC from the transgenic mice; kits comprising several mice, each of which has  
CC a mutation in a different GPCR gene of the invention; and kits comprising  
CC probes which hybridise to GPCR polynucleotides of the invention. The  
CC invention further discloses variants of the GPCR polypeptides and vectors  
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
CC be used in the diagnosis, treatment or prevention of a wide variety of  
CC diseases including neurological disorders (e.g., Alzheimer's disease,  
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
CC disorders of the adrenal gland; disorders of the colon or intestine  
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid

CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
CC uterus, prostate, testis, skin, stomach, spleen, thymus, and  
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
CC nucleic acid of the invention. Note: The full sequence data for this  
CC patent did not form part of the printed specification; those sequences  
CC not shown were obtained in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 906 BP; 173 A; 276 C; 216 G; 241 T; 0 U; 0 Other;  
Query Match 60.3%; Score 604.6; DB 12; Length 906;  
Best Local Similarity 80.8%; Pred. No. 2.2e-154;  
Matches 731; Conservative 0; Mismatches 169; Indels 5; Gaps 2;  
QY 1 ATGGAGAAGGTGGACATGAATACATACAGAGAAACAAGGCTCTGCCAGTTCTCAGAGAAG 60  
DB 1 ATGGAGAGCTAGATATGATGCTCAAGGGTCGTGGCGCCTGCCACTTCTCAGAGAGC 60  
QY 61 TACAAGCAAGTCTACCTCTCCCTGGGCTACAGTATCATCTTTATCTAGGGCTGCCACTA 120  
DB 61 TACAAGCAAGTCTACCTATCATTAACCTACAGTCTCATCTTTATGCTAGGGATGCCCTC 120  
QY 121 AATGGCACTGTCTTGTGGCACTTCTGGGGCCAAACCAAGCGCTGGAGCTGCGCACACC 180  
DB 121 AATGGGGCTGTCTTATGGCTCTCTGGTGCCAAACCAAGCGCTGGAGCTGCGCACCATC 180  
QY 181 TATCTGGTGAACCTGATGGTGGCGGACCTCTTTATGTGCTA---TTGCCCTTCTCTCATC 237  
DB 181 TACTGTATGAACCTGGTGGTGGCTGACCTGCTTTATATGTAAGCCTGCCCTTCTCATC 240  
QY 238 ATCACTTACTCTAGATGACAGGTGGCCCTTCGGGGAGCTGTCTGCAAGCTGGTGCAC 297  
DB 241 ATCACTTACGCGTGGGTGACACCTGGCTCTTTGGGGAGATGCTGTGAGTTGGTGGCG 300  
QY 298 TTCTGTGTTCTATATCAACCTTTAGGCGAGCATCTGCTGCTGACCTGCATCTCTGTGCAC 357  
DB 301 TTCTGTGTTCTACACCAACCTCTACAGCAGCATCTGCTGCTGACCTGCATCTCTACAC 360  
QY 358 CAGTTCCTAGGTGTGTGCCACCCACCTGTGTTCGCTGCCCTACCGGACCCCGCAGGCATGCC 417  
DB 361 CGCTTCTAGAGTGTGCCACCTCTGAGCTCACTGTCTTACCGGACTCAACCGCAGCC 420  
QY 418 TGGCTGGGACACAGCACCTGCGGCCCTGGTGGTCTCTCAGCTGCTGCCACACTGGCC 477  
DB 421 TGGCAGGCACTGCTGCCACCTGGACCCCTGGTAGTCTTCCAAATTGCTGCCGACTCTGGTC 480  
QY 478 TTCTCCACACGCACTACATCAATGGCCAGATGATCTGGTATGACATGACAGCCAAAGAG 537  
DB 481 TTCTCCACACAGCACTATGTAATGGCCAGGTGATCTGATGACAGCCAGCCGAG 540  
QY 538 AATTTTGATCGGCTTTTGGCTACGGCATAGTTCTGACATTGTCTGGCTT--TCTTTCCC 595  
DB 541 CAGTTTGATCATTTCTTCGCTACAGCATAGTACTGAGCTTACTGGGTTGTCTTCCCC 600  
QY 596 TCCTTGTGCTAATTTGGTGTGCTATTACTGATGGTTCAGGAGCCTGATCAAGCCAGAGAG 655  
DB 601 TCCTTGATCATTTCTGGGTGCTACTCTCTGATGGTTCAGGAGCCTGACAAATCCAGTGGAG 660  
QY 656 AACTCATAGGACAGCCACAGCCCGGAGCCAGGTCCATCCGGACCATCTACTCTGTG 715  
DB 661 GACCTCCCAACGACAGGCCACAGCCCGGCAAGTCTATTGGGACATCTCTCTGTG 720  
QY 716 TGTGGCTCTTCAACCTCTCTTTTGTGCCCTTCATATCACTCGCTCTCTTACTCACC 775  
DB 721 TGTGGCTCTTCAACCTCTCTTTTGTGCCCTTCCACATTGCCGATTTCTTACTGATC 780  
QY 776 ATCTGCTTCTGCTTTCTCAGGACTGCGAGCTCTTGATGGCAGCCAGTGTGGCCCTACAAG 835  
DB 781 ATCGCTTCTGAAAGTCACAGGACTGCGAGCTCTTGTGGGCGAGCCAGCATGGCCCTACAAG 840  
QY 836 ATATGGAGGCTCTGTTGATGTTGAGCAGCTGCGCTCAACCCAGTCTCTTCTTTTCA 895

Db 841 GTCTGAGGCCTCTGGTAAGCATGAGCAGCTGGCCTCAATCCAGTCTGTACTTCTTGTCA 900  
Qy 896 AGGGG 900  
Db 901 CAGGG 905

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Job time : 652 secs

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